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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 07:02:52 ; Search time 54 Seconds
(without alignments)
697.626 Million cell updates/sec

Title: US-09-857-841-3

Perfect score: 53
Sequence: 1 gatccatggacaacatctgaa.....gtcgtaccctgcgacgagt 53

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	46	86.8	771	3	US-08-875-233-5	Sequence 5, Appli
2	46	86.8	772	3	US-08-875-233-14	Sequence 14, Appl
3	46	86.8	792	3	US-08-875-233-3	Sequence 3, Appli
4	45	84.9	130	1	US-08-090-193-14	Sequence 14, Appl
5	45	84.9	130	2	US-08-488-031-14	Sequence 14, Appl
6	45	84.9	130	2	US-08-486-569-14	Sequence 14, Appl
7	45	84.9	130	2	US-08-488-027-14	Sequence 14, Appl
8	45	84.9	130	2	US-08-090-192-14	Sequence 14, Appl
9	45	84.9	130	2	US-08-482-663-14	Sequence 14, Appl
10	45	84.9	130	3	US-08-482-658-14	Sequence 14, Appl
11	45	84.9	130	3	US-08-470-349-14	Sequence 14, Appl
12	45	84.9	130	3	US-08-475-610-14	Sequence 14, Appl
13	45	84.9	130	5	PCT-US92-00277-14	Sequence 14, Appl
14	45	84.9	130	5	PCT-US92-00278-14	Sequence 14, Appl
15	45	84.9	131	1	US-08-090-193-11	Sequence 11, Appl
16	45	84.9	131	2	US-08-488-031-11	Sequence 11, Appl
17	45	84.9	131	2	US-08-486-569-11	Sequence 11, Appl
18	45	84.9	131	2	US-08-488-027-11	Sequence 11, Appl
19	45	84.9	131	2	US-08-090-192-11	Sequence 11, Appl
20	45	84.9	131	2	US-08-482-663-11	Sequence 11, Appl
21	45	84.9	131	3	US-08-482-658-11	Sequence 11, Appl
22	45	84.9	131	3	US-08-470-349-11	Sequence 11, Appl
23	45	84.9	131	3	US-08-475-610-11	Sequence 11, Appl
24	45	84.9	131	5	PCT-US92-00277-11	Sequence 11, Appl
25	45	84.9	131	5	PCT-US92-00278-11	Sequence 11, Appl
26	45	84.9	152	1	US-08-090-193-9	Sequence 9, Appli
27	45	84.9	152	2	US-08-488-031-9	Sequence 9, Appli

28	45	84.9	152	2	US-08-486-569-9	Sequence 9, Appli
29	45	84.9	152	2	US-08-488-027-9	Sequence 9, Appli
30	45	84.9	152	2	US-08-090-192-9	Sequence 9, Appli
31	45	84.9	152	2	US-08-482-663-9	Sequence 9, Appli
32	45	84.9	152	3	US-08-482-658-9	Sequence 9, Appli
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35	45	84.9	152	5	PCT-US92-00277-9	Sequence 9, Appli
36	45	84.9	154	1	US-08-090-193-13	Sequence 13, Appl
37	45	84.9	154	2	US-08-488-031-13	Sequence 13, Appl
38	45	84.9	154	2	US-08-486-569-13	Sequence 13, Appl
39	45	84.9	154	2	US-08-488-027-13	Sequence 13, Appl
40	45	84.9	154	2	US-08-090-192-13	Sequence 13, Appl
41	45	84.9	154	2	US-08-482-663-13	Sequence 13, Appl
42	45	84.9	154	3	US-08-482-658-13	Sequence 13, Appl
43	45	84.9	154	3	US-08-470-349-13	Sequence 13, Appl
44	45	84.9	154	3	US-08-475-610-13	Sequence 13, Appl
45	45	84.9	154	5	PCT-US92-00277-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-875-233-5
Sequence 5, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber mosaic virus
STRAIN: V-34
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
OTHER INFORMATION: /codon start= 3
OTHER INFORMATION: /function= "ENCAPSIDATES VIRUS RNA"

OTHER INFORMATION: /product= "COAT PROTEIN"
OTHER INFORMATION: /gene= "Cp"
OTHER INFORMATION: /number= 1
OTHER INFORMATION: /standard_name= "COAT PROTEIN"
US-08-875-233-5

Query Match 86.8%; Score 46; DB 3; Length 771;
Best Local Similarity 100.0%; Pred. No. 5.9e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
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Db 1 CCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46

RESULT 2

US-08-875-233-14
Sequence 14, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: A35
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
US-08-875-233-14

Query Match 86.8%; Score 46; DB 3; Length 772;
Best Local Similarity 100.0%; Pred. No. 5.9e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
Db 1 CCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46

RESULT 3

US-08-875-233-3
Sequence 3, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: v-33
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
US-08-875-233-3

Query Match 86.8%; Score 46; DB 3; Length 792;
Best Local Similarity 100.0%; Pred. No. 5.9e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
Db 1 CCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46

RESULT 4

US-08-090-193-14
Sequence 14, Application US/08090193
Patent No. 5641673
GENERAL INFORMATION:

APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Peritmon, No. 5641673bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
;; STREET: 1100 New York Avenue, Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/090,193
;; FILING DATE: 23-DEC-1993
;; CLASSIFICATION: 514
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/00277
;; FILING DATE: 16-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/642,330
;; FILING DATE: 17-JAN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cimbala, Michele A.
;; REGISTRATION NUMBER: 33,851
;; REFERENCE/DOCKET NUMBER: 0609.3080001
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 130 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;;
;; US-08-090-193-14

Query Match 84.9%; Score 45; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 5
US-08-488-031-14
; Sequence 14, Application US/08488031
; Patent No. 5849548
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perrimon, No. 5849548bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,031
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/090,193
;; FILING DATE: 23-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/00277
;; FILING DATE: 16-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/642,330
;; FILING DATE: 17-JAN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bugaisky, Lawrence B.
;; REGISTRATION NUMBER: 35,086
;; REFERENCE/DOCKET NUMBER: 0609.3080002/MAC/LBB
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 130 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: linear
;;
;; US-08-488-031-14

Query Match 84.9%; Score 45; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 6
US-08-486-569-14
; Sequence 14, Application US/08486569
; Patent No. 5863774
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perrimon, No. 5863774bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,569
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/090,193
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugaisky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3080006/MAC/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
US-08-486-569-14

Query Match 84.9%; Score 45; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||
Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 7

US-08-488-027-14
; Sequence 14, Application US/08488027
; Patent No. 5866384
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perrimon, No. 5866384bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488, 027
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/090,193
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3080003/MAC/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
US-08-488-027-14

Query Match 84.9%; Score 45; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49

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Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 8

US-08-090-192-14
; Sequence 14, Application US/08090192
; Patent No. 5874414
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090,192
; FILING DATE: 11-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/ US 92/00278
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,333
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbal, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0609.3030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-090-192-14

Query Match 84.9%; Score 45; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
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Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 9

US-08-482-663-14
; Sequence 14, Application US/08482663
; Patent No. 5882907
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perrimon, No. 5882907bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,663
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080005/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-482-663-14

Query Match 84.9%; Score 45; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 10
US-08-482-658-14
Sequence 14, Application US/08482658
Patent No. 6010904
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 6010904bert
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193

FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080008/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-482-658-14

Query Match 84.9%; Score 45; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 11
US-08-470-349-14
Sequence 14, Application US/08470349
Patent No. 6015794
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,349
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,192
FILING DATE: 11-NOV-1993
APPLICATION NUMBER: PCT/ US 92/00278
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,333
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-470-349-14

Query Match 84.9%; Score 45; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 12

US-08-475-610-14
Sequence 14, Application US/08475610
Patent No. 6071730
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 6071730bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,610
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080004/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-475-610-14

Query Match 84.9%; Score 45; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 13
PCT-US92-00277-14
Sequence 14, Application PC/TUS9200277

GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, Norbert
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 19920116
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3496604
TELEPHONE: (202)833-7533
TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US92-00277-14

Query Match 84.9%; Score 45; DB 5; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 14
PCT-US92-00278-14
Sequence 14, Application PC/TUS9200278

GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00278
FILING DATE: 19920116
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,333
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3476604
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 833-7533
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Nucleic Acid
PCT-US92-00278-14

Query Match 84.9%; Score 45; DB 5; Length 130;
Best Local Similarity 100.0%; Pred.No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTGACG 49
Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTGACG 96

RESULT 15
US-08-090-193-11
Sequence 11, Application US/08090193
Patent No. 5641673
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5641673bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,193
FILING DATE: 23-DEC-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-090-193-11

Query Match 84.9%; Score 45; DB 1; Length 131;
Best Local Similarity 100.0%; Pred.No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTGACG 49
Db 53 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTGACG 97

Search completed: December 5, 2004, 08:00:07
Job time : 54 secs

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OM protein - protein search, using sw model

Run on: December 5, 2004, 08:05:27 ; Search time 71 Seconds
(without alignments)
70.735 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 14
Sequence: 1 MDKSESTSGRRNR 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	14	3	AAY90255 Ubiquitin
2	14	100.0	218	2	AAR10652 Capsid pr
3	14	100.0	218	2	AAR10653 Capsid pr
4	14	100.0	218	2	AAR57968 Cauliflow
5	14	100.0	218	2	AAR67753 CMV coat
6	14	100.0	218	2	AAR93803 Coat prot
7	14	100.0	218	2	AAR98893 Coat prot
8	14	100.0	218	2	AAR98894 Coat prot
9	14	100.0	218	2	AAR98895 Coat prot
10	12	85.7	218	3	ABR80503 Agrobacte
11	7	50.0	70	4	AAR40661 Propionib
12	7	50.0	70	4	AAR67189 Propionib
13	7	50.0	70	6	ABM63708 Propionib
14	7	50.0	70	6	ABM37180 Propionib
15	7	50.0	107	3	AAG21510 Arabidops
16	7	50.0	147	3	AAG21509 Arabidops
17	7	50.0	147	8	ADN73301 Thale cre
18	7	50.0	175	3	AAG21508 Arabidops
19	6	42.9	15	4	AAB86674 Human cyt
20	6	42.9	15	4	AAB86675 Human cyt
21	6	42.9	15	4	AAB86676 Human cyt
22	6	42.9	15	7	ADL34279 MHC/HLA p
23	6	42.9	15	7	ADL34282 MHC/HLA p
24	6	42.9	15	7	ADL34285 MHC/HLA p
25	6	42.9	15	7	ADL34281 MHC/HLA p

26	6	42.9	15	7	ADL34276 MHC/HLA p
27	6	42.9	15	7	ADL34280 MHC/HLA p
28	6	42.9	15	7	ADL34283 MHC/HLA p
29	6	42.9	15	7	ADL34278 MHC/HLA p
30	6	42.9	15	7	ADL34284 MHC/HLA p
31	6	42.9	15	7	ADL34277 MHC/HLA p
32	6	42.9	20	6	ABJ38036 Human cyt
33	6	42.9	23	5	AAE13475 Peptide #
34	6	42.9	62	4	AAU52188 Propionib
35	6	42.9	62	6	ABM48707 Propionib
36	6	42.9	80	4	AAU91216 Human imm
37	6	42.9	82	7	ABO74002 Pseudomon
38	6	42.9	116	3	AAU03795 Human sec
39	6	42.9	118	2	AAW72060 HSV-2 str
40	6	42.9	146	7	ABO75957 Pseudomon
41	6	42.9	158	4	AAU92693 Human dig
42	6	42.9	180	4	AAU65750 Propionib
43	6	42.9	180	6	ABM62269 Propionib
44	6	42.9	196	3	AAU32144 Human sec
45	6	42.9	203	7	ABO73932 Pseudomon

ALIGNMENTS

RESULT 1	
AAU90255	
ID	AAU90255 standard; protein, 14 AA.
AC	AAU90255;
DT	19-SEP-2000 (first entry)
DE	Ubiquitin monomer C-terminal fragment.
XX	Ubiquitin monomer; protein production; plant cell; ubiquitin promoter.
XX	Nicotiana tabacum.
XX	WO200036129-A1.
XX	22-JUN-2000.
XX	11-DEC-1998; 98WO-SG000103.
XX	11-DEC-1998; 98WO-SG000103.
XX	11-DEC-1998; 98WO-SG000103.
XX	(MOLE-) INST MOLECULAR AGROBIOLOGY.
XX	Fang R, Wu J, Chen X;
XX	WPI; 2000-431604/37.
XX	N-PSDB; AAA30858.
XX	Production of desired protein in plants or plant cells by linking a ubiquitin monomer coding sequence upstream of the gene encoding the desired protein.
XX	Claim 7; Page 18; 42pp; English.
XX	This sequence represents the C-terminal fragment of a ubiquitin monomer. The invention relates to a method for enhancing production of a desired protein in a plant or plant cell by inserting a nucleic acid (NA) encoding a ubiquitin monomer upstream of a NA encoding the desired protein, where the fusion construct encodes a fusion protein and expression is not controlled by the ubiquitin promoter. The invention also relates to a NA acid vector a NA vector able to transform a plant cell, that comprises NA encoding a fusion protein having a ubiquitin monomer linked to a protein of interest and further, where expression of the fusion construct is not under control of a ubiquitin promoter. The construct allows enhanced production of the desired protein in plants or plant cells

SQ Sequence 14 AA;

Query Match 100.0%; Score 14; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGARNRR 14
|||
Db 1 MDKSESTSGARNRR 14

RESULT 2

AAR10652
ID AAR10652 standard; protein; 218 AA.

XX AC AAR10652;

XX DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-APR-1991 (first entry)

XX DE Capsid protein of Cucumber Mosaic Virus strain FNY.

XX KM CMV; resistance; capsid protein; Cucumis melo.

XX OS Cucumber mosaic virus.

XX PN EP412912-A.

XX PD 13-FEB-1991.

XX PF 09-AUG-1990; 90EP-00402282.

XX PR 11-AUG-1989; 89FR-00010848.

XX PA (BIOC-) BIOCEM SA.

XX PI Deboth M, Bentahar S, Noel M, Perret J;

XX WPI; 1991-046027/07.

DR N-PSDB; AAQ10461.

XX PT Transgenic melon plantlets prodn. from transformed shoots - by two=stage
PT culture on specific medium for new transformed plants etc., esp.
PT resistant to cucumber mosaic virus.

XX PS Claim 15; Page 17; 44pp; French.

CC The gene encoding this protein was isolated from a plasmid (pUC18)
CC containing DNA complementary to RNA 3 of the virulent strain FNY,
CC isolated in New York on infected melons. Transgenic melon plantlets
CC containing the nucleotide sequence introduced via an Agrobacterium
CC tumefaciens intermediate are cultured as shoots in special media. The
CC transformed melon plants are resistant to CMV. See also AAQ10462.
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
CC correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 218 AA;

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGARNRR 14
|||
Db 1 MDKSESTSGARNRR 14

RESULT 3

AAR10653
ID AAR10653 standard; protein; 218 AA.

XX AC AAR10653;

XX DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-APR-1991 (first entry)

XX DE Capsid protein of Cucumber Mosaic Virus strain 117F.

XX KM CMV; strain 117F; resistance; capsid protein; Cucumis melo.

XX OS Cucumber mosaic virus.

XX PN EP412912-A.

XX PD 13-FEB-1991.

XX PF 09-AUG-1990; 90EP-00402282.

XX PR 11-AUG-1989; 89FR-00010848.

XX PA (BIOC-) BIOCEM SA.

XX PI Deboth M, Bentahar S, Noel M, Perret J;

XX WPI; 1991-046027/07.

DR N-PSDB; AAQ10462.

XX PT Transgenic melon plantlets prodn. from transformed shoots - by two=stage
PT culture on specific medium for new transformed plants etc., esp.
PT resistant to cucumber mosaic virus.

XX PS Claim 16; Page 19; 44pp; French.

CC The gene encoding this protein was isolated from the virulent French
CC strain 117F of CMV. Transgenic melon plantlets containing the coding
CC sequence (introduced via an Agrobacterium tumefaciens intermediate) are
CC cultured as shoots in special media. The transformed melon plants are
CC resistant to CMV. See also AAQ10461. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC AUG-2003 to correct OS field.)

XX SQ Sequence 218 AA;

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGARNRR 14
|||
Db 1 MDKSESTSGARNRR 14

RESULT 4

AAR57968
ID AAR57968 standard; protein; 218 AA.

XX AC AAR57968;

XX DT 25-MAR-2003 (revised)
DT 20-APR-1995 (first entry)

XX DE Cauliflower mosaic virus capsid protein.

XX KM Cauliflower mosaic virus; CMV; capsid protein; coat protein;
KM polyribzyme; inactivate; inactivation; resistance; crop protection.

XX OS Cauliflower mosaic virus.

XX PN FR2701960-A1.

XX PD 02-SEP-1994.

XX PF 26-FEB-1993; 93FR-00002269.

PR 26-FEB-1993; 93FR-00002269.
XX (GENE-) GENE SHEARS PTY LTD.
XX Lenae P, Perez P, Gruber V, Baudot G, Ollivo C,
XX WPI; 1994-281767/35.
DR N-PSDB; AAQ67395.
XX
XX New polyribozyme contg. several catalytic regions in complementary
PT sequence - can inactivate gene for viral capsid protein, esp. for prepn.
PT of new virus resistant transgenic plants, also DNA sequence encoding it.
XX
XX Disclosure; Fig 2; 67pp; French.
XX
XX The RNA encoding the capsid protein of cauliflower mosaic virus can be
CC targeted by a nucleic acid sequence called a "polyribozyme". The
CC polyribozyme has endoribonuclease activity and is able to inactivate the
CC gene encoding the viral capsid protein. The polyribozyme comprises
CC several catalytic regions derived from ribozymes and confers complete
CC resistance to virus. See AAQ67391-94. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14
Db 1 MDKSESTAGRNRR 14

RESULT 5
AAR67753
ID AAR67753 standard; protein; 218 AA.
XX
AC AAR67753;
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE CMV coat protein.
XX
KM Cucurbit mosaic virus; tomato mosaic virus; minus-strand RNA;
KM virus resistance; disease resistance; transgenic plant; cross protection;
KM hypersensitive response; crop improvement; tomato;
KM Lycopersicon esculentum; tobacco; Nicotiana tabacum; coat protein; CP;
KM TOMV; CMV.
XX
XX Cucurbit mosaic virus.
OS
XX
XX WO9429464-A1.
PN
XX
PD 22-DEC-1994.
XX
XX 03-JUN-1994; 94WO-EP001817.
PF
XX
XX 04-JUN-1993; 93GB-00011593.
PR
XX
XX (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
XX De Haan PT;
PI
XX
XX WPI; 1995-036490/05.
DR N-PSDB; AAQ76106.
XX
XX DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.

XX
PS Disclosure; Page 30; 50pp; English.
XX
XX A chimeric cucumber mosaic virus RNA-3 (given in AAQ76106) codes for the
CC coat protein (CP) of tomato mosaic virus (AAR67552) as well as its own CP
CC (AAR67753). The construct elicits minus-sense RNA that interacts with the
CC RNA-dependent RNA-polymerase of an invading virus, thus conferring virus-
CC resistance on a host plant, e.g. tobacco, tomato. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14
Db 1 MDKSESTAGRNRR 14

RESULT 6
AAR93803
ID AAR93803 standard; protein; 218 AA.
XX
AC AAR93803;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the A35 strain of cucumber mosaic virus.
XX
XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance.
XX
XX Cucurbit mosaic virus; strain A35.
OS
XX
XX WO9621018-A1.
PN
XX
XX 11-JUL-1996.
PD
XX
XX 07-JUN-1995; 95WO-US007234.
PF
XX
XX 30-DEC-1994; 94US-00367789.
PR
XX
XX (ASGR-) ASGROW SEED CO.
PA
XX
XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
PI WPI; 1996-333993/33.
XX
XX N-PSDB; AAT17259.
DR
XX
XX New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
XX Disclosure; Fig 8; 80pp; English.
PS
XX
XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14
Db 1 MDKSESTAGRNRR 14

Db 1 MDKSESTSAGRNR 14

RESULT 7

AAR98893 AAR98893 standard; protein; 218 AA.

XX AAR98893;

DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)

XX Coat protein of the V27 strain of cucumber mosaic virus.

XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KW resistance.

XX Cucumber mosaic virus; strain V27.

XX WO9621018-A1.

XX 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

DR MPI; 1996-333993/33.

DR N-PSDB; AAT34664.

PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.

PS Disclosure; Fig 1; 80pp; English.

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 218 AA;

Query Match 100.0%; Score 14; DB 2; Length 218;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSAGRNR 14

Db 1 MDKSESTSAGRNR 14

RESULT 8

AAR98894 AAR98894 standard; protein; 218 AA.

XX AAR98894;

DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)

XX Coat protein of the V33 strain of cucumber mosaic virus.

XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KW resistance.

XX Cucumber mosaic virus; strain V33.

XX WO9621018-A1.

XX 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

DR MPI; 1996-333993/33.

DR N-PSDB; AAT34665.

PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.

PS Disclosure; Fig 2; 80pp; English.

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 218 AA;

Query Match 100.0%; Score 14; DB 2; Length 218;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSAGRNR 14

Db 1 MDKSESTSAGRNR 14

RESULT 9

AAR98895 AAR98895 standard; protein; 218 AA.

XX AAR98895;

DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)

XX Coat protein of the V34 strain of cucumber mosaic virus.

XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KW resistance.

XX Cucumber mosaic virus; strain V34.

XX WO9621018-A1.

XX 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

DR MPI; 1996-333993/33.

DR N-PSDB; AAT34666.

PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are

PT resistant to infection.
XX
XX Disclosure; Fig 3; 80pp; English.
PS
XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||
Db 1 MDKSESTSAGRNR 14

RESULT 10
ABB80503
ID ABB80503 standard; protein; 218 AA.

XX ABB80503;

DT 25-JUL-2002 (first entry)

DE Agrobacterium tumefaciens protein sequence.

XX Agrobacterium tumefaciens; anti-cucumber mosaic virus; transgenic tomato.

OS Agrobacterium tumefaciens.

PN KR9075101-A.

PD 05-OCT-1999.

PF 17-MAR-1998; 98KR-00009096.

PR 17-MAR-1998; 98KR-00009096.

PA (RURA-) RURAL DEV ADMINISTRATION.

PI Sohn SH, Lee SW, Park JS, Hwang YS;

DR WPI; 2000-577926/54.

DR N-PSDB; ABL58209.

PT Anti-cucumber mosaic virus tomato.

PS Disclosure; Page 4; 6pp; Korean.

XX This sequence represents a protein sequence from Agrobacterium

CC tumefaciens used within the scope of the invention. The invention relates

CC to an anti-cucumber mosaic virus tomato

XX
SQ Sequence 218 AA;

Query Match 85.7%; Score 12; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KSESTTSAGRNR 14
|||
Db 3 KSESTTSAGRNR 14

RESULT 11
AAU40661
ID AAU40661 standard; protein; 70 AA.

XX
AC AAU40661;
XX
DT 13-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #1557.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.

PN WO200181581-A2.

PD 01-NOV-2001.

PF 20-APR-2001; 2001WO-US012865.

PR 21-APR-2000; 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.

XX 07-JUL-2000; 2000US-0216747P.

PA (CORI-) CORIXA CORP.

PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

DR WPI; 2001-616774/71.

DR N-PSDB; AAS59512.

PT Propionibacterium acnes polypeptides and nucleic acids useful for

PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris.

XX
PS Example 1; SEQ ID NO 1856; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

CC polypeptides. The proteins and their associated DNA sequences are used in

CC the treatment, prevention and diagnosis of medical conditions caused by

CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

CC P. acnes is also involved in infections of bone, joints and the central

CC nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the

CC presence or absence of P. acnes in a patient comprises contacting a

CC sample with a binding agent that binds to the proteins of the invention

CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies

CC specific for P. acnes proteins. These antibodies can be used to

CC downregulate expression and activity of P. acnes polypeptides and

CC therefore treat P. acnes infections. The antibodies may also be used as

CC diagnostic agents for determining P. acnes presence, for example, by

CC this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 70 AA;

Query Match 50.0%; Score 7; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SAGRNR 14
|||
Db 52 SAGRNR 58

RESULT 12
AAU67189
ID AAU67189 standard; protein; 70 AA.

```

XX AC AAU67189;
XX DT 27-FEB-2002 (first entry)
XX DE Propionibacterium acnes immunogenic protein #28085.
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX KW dermatological; osteopathic; neuroprotectant.
XX OS Propionibacterium acnes.
XX PN WO200181581-A2.
XX PD 01-NOV-2001.
XX PF 20-APR-2001; 2001WO-US012865.
XX PR 21-APR-2000; 2000US-0199047P.
XX PR 02-JUN-2000; 2000US-0208841P.
XX PR 07-JUL-2000; 2000US-0216747P.
XX PA (CORI-) CORIXA CORP.
XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX DR WPI; 2001-616774/71.
XX DR N-PSDB; AAS59784.
XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
XX PT vaccinating against and diagnosing infections, especially useful for
XX PT treating acne vulgaris.
XX PS Example 1; SEQ ID NO 28384; 1069pp; English.
XX CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX CC polypeptides. The proteins and their associated DNA sequences are used in
XX CC the treatment, prevention and diagnosis of medical conditions caused by
XX CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX CC P. acnes is also involved in infections of bone, joints and the central
XX CC nervous system, however it is particularly involved in the inflammatory
XX CC lesions associated with acne vulgaris. A method for detecting the
XX CC presence or absence of P. acnes in a patient comprises contacting a
XX CC sample with a binding agent that binds to the proteins of the invention
XX CC and determining the amount of bound protein in the sample. The
XX CC polypeptides may be used as antigens in the production of antibodies
XX CC specific for P. acnes proteins. These antibodies can be used to
XX CC downregulate expression and activity of P. acnes polypeptides and
XX CC therefore treat P. acnes infections. The antibodies may also be used as
XX CC diagnostic agents for determining P. acnes presence, for example, by
XX CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
XX CC this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 70 AA;
QY Query Match 50.0%; Score 7; DB 4; Length 70;
QY Best Local Similarity 100.0%; Pred. No. 8.3;
QY Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 8 SAGRNRR 14
Db 52 SAGRNRR 58
```

RESULT 13
ABM63708
ID ABM63708 standard; protein; 70 AA.

```

XX AC ABM63708;
XX DT 20-OCT-2003 (first entry)
XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #28384.
XX KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX KW immunostimulant; immune response; vaccine.
XX OS Propionibacterium acnes.
XX PN WO2003033515-A1.
XX PD 24-APR-2003.
XX PF 11-OCT-2002; 2002WO-US032727.
XX PR 15-OCT-2001; 2001US-00978825.
XX PA (CORI-) CORIXA CORP.
XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
XX PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
XX PI Barth B, Valliee-Douglase J;
XX DR WPI; 2003-381789/36.
XX DR N-PSDB; ACF64713.
XX PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
XX PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX PT or for stimulating an immune response specific for a P. acnes protein.
XX PS Example 1; SEQ ID NO 28384; 1481pp; English.
XX CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
XX CC encoding a Propionibacterium acnes protein. The invention also relates to
XX CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
XX CC immunogenic fragments of P. acnes polypeptides. The invention
XX CC additionally encompasses expression vectors and host cells comprising a
XX CC polynucleotide of the invention; antibodies against polypeptides of the
XX CC invention; fusion proteins comprising a polypeptide of the invention; a
XX CC method for stimulating an immune response specific for a P. acnes
XX CC polypeptide and an isolated T cell population comprising T cells prepared
XX CC via this method; a vaccine composition (comprising P. acnes polypeptides,
XX CC polynucleotides, antibodies, fusion proteins, T cell populations, or
XX CC antigen-presenting cells that express the polypeptide); a method and kit
XX CC for detecting or determining the presence or absence of P. acnes in a
XX CC patient; and a method for inhibiting the development of P. acnes in a
XX CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
XX CC proteins, T cell populations or antigen-presenting cells that express the
XX CC polypeptides are useful for diagnosing, preventing or treating acne
XX CC vulgaris, or for stimulating an immune response specific for a P. acnes
XX CC protein. The polynucleotides can also be used as probes or primers for
XX CC nucleic acid hybridisation. The vaccine composition is useful for the
XX CC stimulation of an immune response against P. acnes, or for treating acne,
XX CC and the kit is useful for performing a diagnostic assay. The present
XX CC sequence represents a polypeptide predicted to be encoded by an ORF (open
XX CC reading frame) contained within the P. acnes polynucleotides of the
XX CC invention. Note: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 70 AA;
QY Query Match 50.0%; Score 7; DB 6; Length 70;
QY Best Local Similarity 100.0%; Pred. No. 8.3;
QY Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 8 SAGRNRR 14
Db 52 SAGRNRR 58
```

RESULT 14
ABM37180
ID ABM37180 standard; protein; 70 AA.
XX
AC ABM37180;
XX
DT 20-OCT-2003 (first entry)
XX
DE Propionibacterium acnes predicted ORF-encoded polypeptide #1856.
XX
KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX immunostimulant; immune response; vaccine.
OS Propionibacterium acnes.
XX
PN WO2003033515-A1.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032727.
XX
PR 15-OCT-2001; 2001US-00978825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallieve-Doulaas J;
XX
XX WPI; 2003-381789/36.
DR N-PSDB; ACF64441.
XX
XX
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX
PS Example 1; SEQ ID NO 1856; 1481bp; English.
XX
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention, antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 70 AA;

Query Match 50.0%; Score 7; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SAGRNRR 14
Db 52 SAGRNRR 58
RESULT 15
AAG21510
ID AAG21510 standard; protein; 107 AA.
XX
AC AAG21510;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24091.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134737P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.

PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 21-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.

PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
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PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
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PR 22-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

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Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KSESTSA 9
Db 96 KSESTSA 102

Search completed: December 5, 2004, 08:15:15
Job time : 74 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 06:39:02 ; Search time 1482 Seconds
(without alignments)
1303.175 Million cell updates/sec

Title: US-09-857-841-3

Perfect score: 53
Sequence: 1 gatccatggacaatctgaa.....gtcgtaccgtcgacgagct 53

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_g881: *
9: gb_g882: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	84.9	127	4	BM067231 KS08001E1
2	20	37.7	287	2	BM440162 BB440162
3	18	34.0	288	2	BB006007 BB006007
4	18	34.0	316	2	BB494132 BB494132
5	18	34.0	428	6	CA016832 HV05N02u
6	18	34.0	500	6	CA017649 HV05N02r
7	18	34.0	597	5	BQ595418 E012691-0
8	18	34.0	608	4	BM333093 MEST183-H
9	18	34.0	611	4	BM347598 MEST279-G
10	18	34.0	627	9	AG223668 LotuS cor
11	18	34.0	629	4	BI271889 NF014E05F
12	18	34.0	688	5	BX752014 BX752014
13	18	34.0	688	7	CK185060 EST774375
14	18	34.0	701	6	CB634510 OS11Eb14B
15	18	34.0	713	9	CC501966 CH240_340
16	18	34.0	735	6	CB618020 OS11Ea01J
17	18	34.0	742	5	BX874992 BX874992
18	18	34.0	742	9	AG379970 Mus muscu
19	18	34.0	760	6	CB618065 OS11Ea01K
20	18	34.0	778	7	CK190493 EST779808
21	18	34.0	816	9	CC708428 OGULP54TV
22	18	34.0	833	4	BG299724 HVSMEa002
23	18	34.0	877	6	CB622656 OS11Ea09K
24	18	34.0	881	5	BX749432 BX749432

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	26	18	34.0	915	9	CC708421	CC708421	OGULP54TH
	27	18	34.0	959	2	BE421380	BE421380	HWM008.GO
	28	18	34.0	971	9	CG281990	CG281990	OG3DG39TH
	29	17	32.1	251	1	AV246895	AV246895	AV246895
	30	17	32.1	268	2	BB087806	BB087806	BB087806
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	35	17	32.1	669	1	AL651847	AL651847	AL651847
	36	17	32.1	687	9	AG179628	AG179628	Pan trogl
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	38	17	32.1	720	7	CK183518	CK183518	EST772833
	39	17	32.1	773	9	BX240998	BX240998	Danio rer
	40	17	32.1	824	8	CC431250	CC431250	PUEFG48TD
	41	17	32.1	844	8	CC407226	CC407226	PUEEQ91TD
	42	17	32.1	846	9	CL563987	CL563987	OB_Ba002
	43	17	32.1	930	8	BZ667152	BZ667152	PUBDF19TD
	44	17	32.1	973	3	AY068889	AY068889	Schmidtea
	45	17	32.1	980	9	CNS0650W	AL401862	T7 end of

ALIGNMENTS

RESULT 1
LOCUS BM067231 127 bp mRNA linear EST 11-SEP-2002
DEFINITION KS08001E12 KS08 Capsicum annuum cDNA, mRNA sequence.
ACCESSION BM067231
VERSION BM067231.1 GI:22787366
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Capsicum.

REFERENCE 1 (bases 1 to 127)
Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S.,
Hur, C.-G. and Choi, D.

AUTHORS

Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
annuum L.) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen
Unpublished (2001)

JOURNAL

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Genome Research Center and National Center for Genome Information
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Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doll@mail.kribb.re.kr

COMMENT

High quality sequence stop: 127.
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/note="Vector: pBluescript SK(-)"

FEATURES

source

ORIGIN

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Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 CATGACAAATCTGATCAACCACTGCTGCTGTAACCGTCAAG 49
79 CATGACAAATCTGATCAACCACTGCTGCTGTAACCGTCAAG 35

RESULT 2
BB440162
LOCUS
DEFINITION BB440162 RIKEN full-length enriched, 9 days embryo Mus musculus
CDNA clone D030020106 3' similar to U19932 Mouse (beta ig-h3) mRNA,
mRNA sequence.
ACCESSION BB440162
VERSION BB440162.1 GI:9282774
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermostabilization of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
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Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
source
1. .287
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand CDNA was
primed with a primer [5',
GAGAGAGAGCGCGCGCACTGAGTTTCTTTTCTTTTCTT 3'], CDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand CDNA was prepared with the

primer adapter of sequence [5'
GAGAGAGATTCCTCGAGTTAATTAATTAATTCCTCCCCCCCCCCCC 3']. CDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLX I."

ORIGIN
Query Match 37.7%; Score 20; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 ACAAACTGAATCAACCACT 29
47 ACAAACTGAATCAACCACT 66
Db

RESULT 3
BB006007
LOCUS
DEFINITION BB006007 288 bp mRNA linear EST 22-JUN-2000
BB006007 RIKEN full-length enriched, 10 day neonate skin Mus
musculus CDNA clone 4732469F24 3' similar to NM_009369 Mus musculus
transforming growth factor, beta induced, 68 kDa (Tgfb1), mRNA
sequence.
ACCESSION BB006007
VERSION BB006007.1 GI:8095422
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermostabilization of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
source
1. .288
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/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTTTT TTT TTT TTT TTT V N 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAAATTATCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"

ORIGIN

Query Match 34.0%; Score 18; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ACAATCTGAATCAACCA 27
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Db 37 ACAATCTGAATCAACCA 54

RESULT 4 316 bp mRNA linear EST 25-JUL-2000
BB494132 RIKEN full-length enriched, 13 days embryo stomach Mus
LOCUS BB494132 CDNA clone D530037K16 3' similar to l19932 Mouse (beta
DEFINITION 1g-h3) mRNA, mRNA sequence.

ACCESSION BB494132 GI:9452759
VERSION BB494132.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 316)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
Takahashi,F., Tomnaga,N., Toya,T., Tsunoda,Y., Wachihi,A.,
Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.

TITLE RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL Unpublished (2000)
COMMENT Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
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Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
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Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.

FEATURES

source

location/Qualifiers
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/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGCGCGCACTCGAGTTT TTT TTT TTT TTT V N 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATTCGAGTTAATTAAATTATCCCCCCCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 34.0%; Score 18; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ACAATCTGAATCAACCA 27
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Db 65 ACAATCTGAATCAACCA 82

RESULT 5
CA016832/c

LOCUS CA016832 428 bp mRNA linear EST 23-OCT-2002
DEFINITION HV05N02u HV Hordeum vulgare subsp. vulgare CDNA clone HV05N02
3-PRIME, mRNA sequence.

ACCESSION CA016832
VERSION CA016832.1 GI:24294176
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 428)
AUTHORS Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and
Graner,A.

TITLE Barley ESTs from germinating seeds
JOURNAL Unpublished (2002)
COMMENT Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)

Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
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Plate: 5 row: N column: 2
Seq primer: M13uni.

FEATURES
source

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/lab_host="XL10-Gold"
/clone_lib="HV"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Roots were grown for two days on filter paper at room temperature. Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable.Average insert size is 1 kb"

ORIGIN

Query Match 34.0%; Score 18; DB 6; Length 428;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AAATCTGAATCAACCACT 29
|||||
Db 198 AAATCTGAATCAACCACT 181

RESULT 6
CA017649 500 bp mRNA linear EST 23-OCT-2002
LOCUS HV05N02r HV Hordeum vulgare subsp. vulgare cDNA clone HV05N02
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION CA017649
VERSION CA017649.1 GI:24294993
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae; Triticeae; Hordeum.
1 (bases 1 to 500)
Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and Graner,A.
TITLE Barley ESTs from germinating seeds
JOURNAL Unpublished (2002)
COMMENT Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 500 Std Error: 0.00
Plate: 5 row: N column: 2
Seq primer: M13rev.

FEATURES
source
1. .500
Location/Qualifiers
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"

/cultivar="barke"
/sub_species="vulgare"
/db_xref="GABI:267679"
/db_xref="taxon:112509"
/clone="HV05N02"
/tissue_type="germinating seeds"
/dev_stage="germinating seeds (48-96 h)"
/lab_host="XL10-Gold"
/clone_lib="HV"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Roots were grown for two days on filter paper at room temperature. Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable.Average insert size is 1 kb"

ORIGIN

Query Match 34.0%; Score 18; DB 6; Length 500;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AAATCTGAATCAACCACT 29
|||||
Db 452 AAATCTGAATCAACCACT 469

RESULT 7
BQ595418 597 bp mRNA linear EST 06-DEC-2002
LOCUS E012691-024-022-C22-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
DEFINITION CDNA clone 024-022-C22 5-PRIME, mRNA sequence.
ACCESSION BQ595418
VERSION BQ595418.1 GI:26125001
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 597)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 597 Std Error: 0.00
Plate: 22 row: C column: 22
Seq primer: SP6; CATACGATTGAGTGACACTATAG.

FEATURES
source
1. .597
Location/Qualifiers
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:191436"
/db_xref="taxon:161934"
/clone="024-022-C22"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-developing root"

/note=Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

ORIGIN

Query Match 34.0%; Score 18; DB 5; Length 597;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AATCTGATCAACCACTG 30
|||||
Db 145 AATCTGAATCAACCACTG 162

RESULT 8
BM333093/c 608 bp mRNA linear EST 16-JAN-2002
LOCUS MEST183-H08.T3 ISUM5-RN Zea mays cDNA clone MEST183-H08 3', mRNA
DEFINITION
sequence.
ACCESSION BM333093
VERSION BM333093.1 GI:18163254
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Men,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
TITLE Expressed Sequence Tags from B73 Maize: various stages and tissues
including seedlings treated with a variety of hormones
JOURNAL Unpublished (2001)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basacall and confidence value were assigned using the
Phred software,
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b>
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES

source
1. 608
/organism="Zea mays"
/mol_type="mRNA"
/cultiVar="B73"
/db_xref="taxon:4577"
/clone="MEST183-H08"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_lib="ISUM5-RN"
/note=Vector: PT7T3PAC; Site_1: EcoRI; Site_2: NotI;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels

(3, 5, 10, 15, 20, 25, 30, DAG), Adventitious roots (65
DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear
(0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk,
unpollinated, first ear, ear shank, etiolated seedlings,
callus, Cycloheximide-treated callus, Anaerobic treated
seedlings, NAA (a-Naphthalene acetic acid)-treated
seedlings, Kinetin-treated seedlings, ACPG
(1-aminocyclopropane-1-carboxylic acid)-treated seedlings,
Brassinolide-treated seedlings, ABA (Abscissic
acid)-treated seedlings, GA (Gibberellic acid)-treated
seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA
molecules were generated as follows. First-strand cDNA was
prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT primer (5'
AACTGAGAAGATTGCGCGCCGACGAATTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT7T3PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

ORIGIN

Query Match 34.0%; Score 18; DB 4; Length 608;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATCAACCACTGCTG 34
|||||
Db 317 TGAATCAACCACTGCTG 300

RESULT 9
BM347598/c 611 bp mRNA linear EST 16-JAN-2002
LOCUS MEST279-G08.T3 ISUM5-RN Zea mays cDNA clone MEST279-G08 3', mRNA
DEFINITION
sequence.
ACCESSION BM347598
VERSION BM347598.1 GI:18172210
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Men,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
TITLE Expressed Sequence Tags from B73 Maize: various stages and tissues
including seedlings treated with a variety of hormones
JOURNAL Unpublished (2001)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basacall and confidence value were assigned using the
Phred software,
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b>
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)

FEATURES

source
1. 608
/organism="Zea mays"
/mol_type="mRNA"
/cultiVar="B73"
/db_xref="taxon:4577"
/clone="MEST183-H08"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_lib="ISUM5-RN"
/note=Vector: PT7T3PAC; Site_1: EcoRI; Site_2: NotI;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels

XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

ORIGIN

Query Match 34.0%; Score 18; DB 4; Length 629;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GATCCATGACAAATCTG 18
|||||
Db 108 GATCCATGACAAATCTG 91

RESULT 12

BX752014 688 bp mRNA linear EST 09-DEC-2003
LOCUS BX752014 XGC-gastrula Xenopus tropicalis cDNA clone TGas076c13 3',
DEFINITION mRNA sequence.

ACCESSION BX752014 GI:39642082
VERSION BX752014
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
TITLE Xenopodinae; Xenopus; Silurana.
JOURNAL 1 (bases 1 to 688)

COMMENT Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas076c13.q1kT7
Sequencing primer: T7

This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13
gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers

FEATURES
Source 1..688
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TGas076c13"
/dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-gastrula"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."

ORIGIN

Query Match 34.0%; Score 18; DB 5; Length 688;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TCCATGACAAATCTGAA 20
|||||
Db 332 TCCATGACAAATCTGAA 349

RESULT 13

CK185060 688 bp mRNA linear EST 01-JUL-2004
LOCUS CK185060
DEFINITION EST774375 BEA Boophilus microplus cDNA clone BEAC260, mRNA

sequence.
CK185060
CK185060.1 GI:49565594
EST.
Boophilus microplus (southern cattle tick)

REFERENCE Nene, V., Quackenbush, J., George, J. and Guerrero, F.
AUTHORS An index of genes transcribed in the tick Boophilus microplus
TITLE Unpublished (2004)
JOURNAL Other ESTs: EST774376
COMMENT Contact: Vishvanath Nene
Parasite Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-610-5968
Fax: 301-838-0208
Email: nene@tigr.org
Seq primer: M13 forward.

FEATURES
source Location/Qualifiers
1..688
/organism="Boophilus microplus"
/mol_type="mRNA"
/db_xref="taxon:6941"
/clone="BEAC260"
/dev_stage="Adult and larvae"
/lab_host="E. coli strain DH10B-Tona"
/clone_lib="BEA"
/note="Organ: whole ticks and dissected organs; Vector:
pExpress 1; A normalized cDNA library was custom built by
Express Genomics. Oligo-dT primed cDNA was directionally
cloned into NotI-EcoRV site of pExpress 1. Universal M13
primers were used to generate 5' and 3' EST data."

ORIGIN

Query Match 34.0%; Score 18; DB 7; Length 688;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 34 GTCGTAAACCGTCGACGAG 51
|||||
Db 45 GTCGTAAACCGTCGACGAG 62

RESULT 14
CB634510/c 701 bp mRNA linear EST 08-APR-2003
LOCUS OS11EB14B06.f OS11EB Oryza sativa (indica cultivar-group) cDNA
DEFINITION clone OS11EB14B06 5', mRNA sequence.
ACCESSION CB634510
VERSION CB634510.1 GI:29629501
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Eukaryota; Magnoliopsida; Liliopsida; Poales; Poaceae;
TITLE Spermatophyta; Oryzae; Oryza.
JOURNAL 1 (bases 1 to 701)
COMMENT Jantaasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: B column: 06
Seq primer: gta aaa cga cgg cca gtc.
Location/Qualifiers

1. .701
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
/db_xref="taxon:39946"
/clone="OS1EB14B06"
/issue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OS1EB"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after inoculation with Rice Blast (PO6-6-3)"

Query Match 34.0%; Score 18; DB 6; Length 701;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATGACAAATCTGAATCA 23
|||||
DB 586 ATGACAAATCTGAATCA 569

RESULT 15
CC501966/c
LOCUS 713 bp DNA linear GSS 17-JUN-2003
DEFINITION CH240_340H21.T7 CHORI-240 Bos taurus genomic clone CH240_340H21,
genomic survey sequence.
ACCESSION CC501966
VERSION CC501966.1 GI:31820259
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE 1 (bases 1 to 713)
AUTHORS Holt,R., Scott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Tsai,M., Cloutier,A., Lee,D., Glyn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
Dalrymple,B.P. and Tellam,R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other_GSSs: CH240_340H21.TARBAC13P2
COMMENT Contact: Rob Holt

Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-6276

EMAIL: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pletier de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 340 row: H column: 21
Seq primer: T7

FEATURES
Source 1. .713
Location/Qualifiers
/organism="Bos taurus"

/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_340H21"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: PTARBAC1.3; Site_1: MboI; Site_2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pletier de Jong"

Query Match 34.0%; Score 18; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TGGACAAATCTGAATCAA 24
|||||
DB 413 TGGACAAATCTGAATCAA 396

Search completed: December 5, 2004, 07:59:11
Job time : 1487 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 06:38:07 ; Search time 1425 Seconds
(without alignments)
1758.845 Million cell updates/sec

Title: US-09-857-841-3

Perfect score: 53
Sequence: 1 gatccatgacaatctgaa.....gtcgtaacgcgtcgacgagct 53

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_hcg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	53	100.0	53	6	BD261798
2	46	86.8	771	6	AR111976
3	46	86.8	772	6	AR111981
4	46	86.8	792	6	AR111975
5	45	84.9	130	6	AR031575
6	45	84.9	130	6	AR065687
7	45	84.9	130	6	AR097446
8	45	84.9	130	6	I49964
9	45	84.9	131	6	AR031572
10	45	84.9	131	6	AR065684
11	45	84.9	131	6	AR097443
12	45	84.9	131	6	I49961
13	45	84.9	152	6	AR031570
14	45	84.9	152	6	AR065682
15	45	84.9	152	6	AR097441
16	45	84.9	152	6	I49959
17	45	84.9	154	6	AR031574
18	45	84.9	154	6	AR065686
19	45	84.9	154	6	AR097445

20	45	84.9	154	6	I49963	I49963 Sequence 13
21	45	84.9	862	14	CMU32859	U32859 Cucumbe mo
22	45	84.9	864	14	CMU32858	U32858 Cucumbe mo
23	45	84.9	894	14	MCVCPB	I36525 Cucumbe mo
24	45	84.9	976	6	A32131	A32131 CMV capsid
25	45	84.9	976	6	AR021486	AR021486 Sequence
26	45	84.9	976	6	AR138342	AR138342 Sequence
27	45	84.9	976	6	AR364710	AR364710 Sequence
28	45	84.9	976	6	BD000278	BD000278 Transgeni
29	45	84.9	1007	6	A32133	A32133 CMV capsid
30	45	84.9	1007	6	A39812	A39812 Sequence 6
31	45	84.9	1007	6	AR021487	AR021487 Sequence
32	45	84.9	1007	6	AR138343	AR138343 Sequence
33	45	84.9	1007	6	AR364711	AR364711 Sequence
34	45	84.9	1007	6	AR430190	AR430190 Sequence
35	45	84.9	1007	6	BD000279	BD000279 Transgeni
36	45	84.9	1007	14	CUMCVRN4	X16386 Cucumbe mo
37	45	84.9	1033	14	CMU22821	U22821 Cucumbe mo
38	45	84.9	1043	14	CMVCOATP	X77855 Cucumbe mo
39	45	84.9	1066	6	A67212	A67212 Sequence 1
40	45	84.9	1067	6	AR076864	AR076864 Sequence
41	45	84.9	1113	14	CMO131624	AJ131624 Cucumbe
42	45	84.9	1115	14	CMO131623	AJ131623 Cucumbe
43	45	84.9	1362	14	MCVCPA	M22710 Cucumbe mo
44	45	84.9	1379	6	E01821	E01821 cDNA encodi
45	45	84.9	1696	6	A41823	A41823 Sequence 4

ALIGNMENTS

RESULT 1	BD261798	53 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD261798	Enhancement in protein production by higher plants using ubiquitin			
DEFINITION	BD261798	Enhancement in protein production by higher plants using ubiquitin			
ACCESSION	BD261798.1	GI:33071566			
VERSION	JP 2002532098-A/2.				
KEYWORDS	Cucumber mosaic virus (cucumber mosaic cucumovirus)				
SOURCE	Cucumber mosaic virus				
ORGANISM	Vituses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae; Cucumovirus.				
REFERENCE	1 (bases 1 to 53)				
AUTHORS	Fang,R.X., Wu,J.L. and Chen,X.Y.				
TITLE	Enhancement in protein production by higher plants using ubiquitin				
JOURNAL	or cucumber mosaic virus coating protein peptide				
COMMENT	Patent: JP 2002532098-A 2 02-OCT-2002;				
	INSTITUTE OF MOLECULAR AGROBIOLOGY				
	OS Cucumber mosaic virus				
	PN JP 2002532098-A/2				
	PD 02-OCT-2002				
	PF 11-DEC-1998 JP 2000588378				
	PI RONG XIANG FANG,JUNG LIN WU,XIAO YING CHEN				
	PC C12N15/09,A01H5/00,C07K14/415,C07K19/00,C12N5/10,C12N15/00, PC				
	C12N5/00				
FEATURES	CC Enhancement in protein production by higher plants using				
Source	ubiquitin or				
	CC cucumber mosaic virus coating protein peptide FH Key				
	location/Qualifiers				
	FT CDS (6)..(47).				
	location/Qualifiers				
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	/mol_type="genomic DNA"				
	/db_xref="taxon:12305"				
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Best Local Similarity	100.0%; Pred. No. 2.2e-20;				
Matches	53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	1 GATCCATGACAATCTGAATCAACGAGTGTGCTGTAACCGTCGACGAGCT 53				

James

Db 1 GATCCATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACGAGCT 53
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RESULT 2
AR111976
LOCUS AR111976 771 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6127601.
ACCESSION AR111976
VERSION AR111976.1 GI:12828824
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 771)
Boeshore,M.L., McMaster,R.J., Tricoli,D.M., Reynolds,J.F. and
AUTHORS Carney,K.J.
TITLE Plants resistant to C strains of cucumber mosaic virus
JOURNAL Patent: US 6127601-A 5 03-OCT-2000;
FEATURES
location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 3.6e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CCATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 46
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RESULT 3
AR111981
LOCUS AR111981 772 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 14 from patent US 6127601.
ACCESSION AR111981
VERSION AR111981.1 GI:12828829
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 772)
Boeshore,M.L., McMaster,R.J., Tricoli,D.M., Reynolds,J.F. and
AUTHORS Carney,K.J.
TITLE Plants resistant to C strains of cucumber mosaic virus
JOURNAL Patent: US 6127601-A 14 03-OCT-2000;
FEATURES
location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 3.6e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CCATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 49
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RESULT 4
AR111975
LOCUS AR111975 792 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6127601.
ACCESSION AR111975
VERSION AR111975.1 GI:12828823
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 792)
Boeshore,M.L., McMaster,R.J., Tricoli,D.M., Reynolds,J.F. and
AUTHORS Carney,K.J.
TITLE Plants resistant to C strains of cucumber mosaic virus
JOURNAL Patent: US 6127601-A 3 03-OCT-2000;
FEATURES
location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 3.6e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5
AR031575
LOCUS AR031575 130 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5866384.
ACCESSION AR031575
VERSION AR031575.1 GI:5945864
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 130)
Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
AUTHORS Cell ablation using trans-splicing ribozymes
TITLE Patent: US 5866384-A 14 02-FEB-1999;
JOURNAL location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 49
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Db 52 CATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 96
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RESULT 6
AR065687
LOCUS AR065687 130 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5849548.
ACCESSION AR065687
VERSION AR065687.1 GI:5995903
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 130)
Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
AUTHORS Cell ablation using trans-splicing ribozymes
TITLE Patent: US 5849548-A 14 15-DEC-1998;
JOURNAL location/Qualifiers
1..130
/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 84.9%; Score 45; DB 6; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 7
AR097446 130 bp DNA linear PAT 14-FEB-2001
LOCUS AR097446
DEFINITION Sequence 14 from patent US 6071730.
ACCESSION AR097446
VERSION AR097446.1 GI:12806176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 14 06-JUN-2000;
FEATURES
location/Qualifiers
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Query Match 84.9%; Score 45; DB 6; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
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Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 8
149964 130 bp DNA linear PAT 07-OCT-1997
LOCUS 149964
DEFINITION Sequence 14 from patent US 5641673.
ACCESSION 149964
VERSION 149964.1 GI:2472184
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5641673-A 14 24-JUN-1997;
FEATURES
location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
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Db 52 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 9
AR031572 131 bp DNA linear PAT 29-SEP-1999
LOCUS AR031572
DEFINITION Sequence 11 from patent US 5866384.
ACCESSION AR031572
VERSION AR031572.1 GI:5945861
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 11 02-FEB-1999;
FEATURES
location/Qualifiers
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/mol_type="unassigned DNA"

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Query Match 84.9%; Score 45; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
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Db 53 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 97

RESULT 10
AR065684 131 bp DNA linear PAT 29-SEP-1999
LOCUS AR065684
DEFINITION Sequence 11 from patent US 5849548.
ACCESSION AR065684
VERSION AR065684.1 GI:5995900
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 11 15-DEC-1998;
FEATURES
location/Qualifiers
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ORIGIN
Query Match 84.9%; Score 45; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
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QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
Db 53 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 97

RESULT 11
AR097443 131 bp DNA linear PAT 14-FEB-2001
LOCUS AR097443
DEFINITION Sequence 11 from patent US 6071730.
ACCESSION AR097443
VERSION AR097443.1 GI:12806173
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 11 06-JUN-2000;
FEATURES
location/Qualifiers
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/mol_type="unassigned DNA"

ORIGIN
Query Match 84.9%; Score 45; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGCTAACCCTGACG 49
|||||
Db 53 CATGACAAATCTGAATCAACCAAGTGTGCTGCTAACCCTGACG 97

RESULT 12

LOCUS 149961 131 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 11 from patent US 5641673.
ACCESSION I49961
VERSION I49961.1 GI:2472181
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5641673-A 11 24-JUN-1997;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 84.9%; Score 45; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGCTAACCCTGACG 49
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Db 53 CATGACAAATCTGAATCAACCAAGTGTGCTGCTAACCCTGACG 97

RESULT 13

LOCUS AR031570 152 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5866384.
ACCESSION AR031570
VERSION AR031570.1 GI:5945859
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 9 02-FEB-1999;
FEATURES Location/Qualifiers
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Query Match 84.9%; Score 45; DB 6; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGCTAACCCTGACG 49
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Db 74 CATGACAAATCTGAATCAACCAAGTGTGCTGCTAACCCTGACG 118

RESULT 14

LOCUS AR065682 152 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5849548.
ACCESSION AR065682
VERSION AR065682.1 GI:5995898
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 9 15-DEC-1998;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 9 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..152
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 84.9%; Score 45; DB 6; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGCTAACCCTGACG 49
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Db 74 CATGACAAATCTGAATCAACCAAGTGTGCTGCTAACCCTGACG 118

RESULT 15

LOCUS AR097441 152 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6071730.
ACCESSION AR097441
VERSION AR097441.1 GI:12806171
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 9 06-JUN-2000;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 84.9%; Score 45; DB 6; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGCTAACCCTGACG 49
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Db 74 CATGACAAATCTGAATCAACCAAGTGTGCTGCTAACCCTGACG 118

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Job time : 1425 secs

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 07:06:47 ; Search time 228 Seconds
(without alignments)
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Title: US-09-857-841-3

Perfect score: 53

Sequence: 1 gatccatggacaatctgaa.....gtcgtaccgtcgacgagct 53

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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	86.8	771	US-10-011-033-5	Sequence 5, Appli
2	46	86.8	772	US-10-011-033-14	Sequence 14, Appli
3	46	86.8	792	US-10-011-033-3	Sequence 3, Appli
4	43	81.1	772	US-10-011-033-1	Sequence 1, Appli
5	37	69.8	960	US-10-011-033-9	Sequence 9, Appli
6	20	37.7	1674	US-10-369-493-35833	Sequence 35833, A
7	18	34.0	1020	US-10-425-115-38826	Sequence 38826, A
8	18	34.0	1116	US-10-156-761-6291	Sequence 6291, Ap
9	18	34.0	1996	US-10-424-599-94969	Sequence 94969, A
10	18	34.0	3878	US-10-101-464A-950	Sequence 950, App
11	18	34.0	9025608	US-10-156-761-1	Sequence 1, Appli
12	17	32.1	285	US-10-437-963-97141	Sequence 97141, A

13	17	32.1	762	13	US-10-027-632-3534	Sequence 3534, Ap
14	17	32.1	762	13	US-10-027-632-3535	Sequence 3535, Ap
15	17	32.1	762	13	US-10-027-632-3536	Sequence 3536, Ap
16	17	32.1	762	15	US-10-027-632-3534	Sequence 3534, Ap
17	17	32.1	762	15	US-10-027-632-3535	Sequence 3535, Ap
18	17	32.1	762	15	US-10-027-632-3536	Sequence 3536, Ap
19	17	32.1	28854	9	US-09-741-151-3	Sequence 3, Appli
20	16	30.2	527	17	US-10-767-701-22640	Sequence 22640, A
21	16	30.2	707	16	US-10-424-599-105422	Sequence 105422, A
22	16	30.2	713	13	US-10-027-632-21126	Sequence 21126, A
23	16	30.2	713	15	US-10-027-632-21126	Sequence 21126, A
24	16	30.2	744	13	US-10-027-632-20862	Sequence 20862, A
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26	16	30.2	824	17	US-10-767-701-5419	Sequence 5419, Ap
27	16	30.2	2621	16	US-10-424-599-76572	Sequence 76572, A
28	16	30.2	4116	15	US-10-296-540-3	Sequence 3, Appli
29	16	30.2	4116	17	US-10-296-450A-3	Sequence 3, Appli
30	16	30.2	11476	16	US-10-434-893A-3	Sequence 3, Appli
31	15	28.3	145	9	US-09-864-761-17367	Sequence 17367, A
32	15	28.3	246	18	US-10-425-115-101455	Sequence 101455, A
33	15	28.3	390	17	US-10-437-963-25065	Sequence 25065, A
34	15	28.3	402	17	US-10-437-963-74167	Sequence 74167, A
35	15	28.3	419	17	US-10-767-795-560	Sequence 560, App
36	15	28.3	441	18	US-10-425-115-90059	Sequence 90059, A
37	15	28.3	449	14	US-10-060-036-3474	Sequence 3474, Ap
38	15	28.3	449	14	US-10-060-036-4108	Sequence 4108, Ap
39	15	28.3	472	16	US-10-424-599-29886	Sequence 29886, A
40	15	28.3	480	11	US-09-876-143-658	Sequence 658, App
41	15	28.3	508	15	US-10-029-386-1276	Sequence 1276, Ap
42	15	28.3	517	14	US-10-060-036-3938	Sequence 3938, Ap
43	15	28.3	517	17	US-10-767-701-1327	Sequence 1327, Ap
44	15	28.3	520	13	US-10-027-632-18852	Sequence 18852, A
45	15	28.3	520	15	US-10-027-632-18852	Sequence 18852, A

ALIGNMENTS

RESULT 1
US-10-011-033-5
; Sequence 5, Application US/10011033
; Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber mosaic virus
STRAIN: V-34
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
OTHER INFORMATION: /codon_start= 3
/function= "ENCAPSIDATES VIRUS RNA"
/product= "COAT PROTEIN"
/gene= "Cp"
/number= 1
/standard_name= "COAT PROTEIN"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-011-033-5

Query Match 86.8%; Score 46; DB 13; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCATGGACAAATCTGAATCAACCACTGCTGTCGTAACCGTCGACG 49
Db 1 CCATGGACAAATCTGAATCAACCACTGCTGTCGTAACCGTCGACG 46

RESULT 2
US-10-011-033-14
Sequence 14, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: A35
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-011-033-14

Query Match 86.8%; Score 46; DB 13; Length 772;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCATGGACAAATCTGAATCAACCACTGCTGTCGTAACCGTCGACG 49
Db 1 CCATGGACAAATCTGAATCAACCACTGCTGTCGTAACCGTCGACG 46

RESULT 3
US-10-011-033-3
Sequence 3, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS

STRAIN: v-33
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-011-033-3

Query Match 86.8%; Score 46; DB 13; length 792;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCATGACAAATCTGAATCAACGAGTGTGCTGTAACCGTGACG 49
1 CCATGACAAATCTGAATCAACGAGTGTGCTGTAACCGTGACG 46

RESULT 4
US-10-011-033-1

Sequence 1, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: V-27

FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-011-033-1

Query Match 81.1%; Score 43; DB 13; length 772;
Best Local Similarity 100.0%; Pred. No. 8.9e-15;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 CCATGACAAATCTGAATCAACGAGTGTGCTGTAACCGTCG 46
1 CCATGACAAATCTGAATCAACGAGTGTGCTGTAACCGTCG 43

RESULT 5
US-10-011-033-9

Sequence 9, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: STRAIN C

FEATURE:
NAME/KEY: CDS
LOCATION: 1..658
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-011-033-9

Query Match 69.8%; Score 37; DB 13; length 960;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 ATGACAAATCTGAATCAACGAGTGTGCTGTAACC 42
1 ATGACAAATCTGAATCAACGAGTGTGCTGTAACC 37

RESULT 6
US-10-369-493-35833/c

; Sequence 35833, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35833
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35833

Query Match 37.7%; Score 20; DB 15; Length 1674;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GTGCTGCTCGTAACCGTCGA 47
|||||
Db 1278 GTGCTGCTCGTAACCGTCGA 1259

RESULT 7
US-10-425-115-38826
; Sequence 38826, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 38826
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_135411C.1
US-10-425-115-38826

Query Match 34.0%; Score 18; DB 18; Length 1020;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATCAACCGTGTGG 34
|||||
Db 983 TGAATCAACCGTGTGG 1000

RESULT 8
US-10-156-761-6291/c
; Sequence 6291, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6291
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1116)
US-10-156-761-6291

Query Match 34.0%; Score 18; DB 15; Length 1116;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TGCTGTGCTGAACCGTCG 46
|||||
Db 185 TGCTGTGCTGAACCGTCG 168

RESULT 9
US-10-424-599-94969
; Sequence 94969, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 94969
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_56769C.1
US-10-424-599-94969

Query Match 34.0%; Score 18; DB 16; Length 1996;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GGTGTAACCGTCGACGA 50
|||||
Db 532 GGTGTAACCGTCGACGA 549

RESULT 10
US-10-101-464A-950/c
; Sequence 950, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A

; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 950
; LENGTH: 3878
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; US-10-101-464A-950

Query Match 34.0%; Score 18; DB 14; Length 3878;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 ATGACAAATCTGAATCA 23
DB 2685 ATGACAAATCTGAATCA 2668

RESULT 11

US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
; US-10-156-761-1

Query Match 34.0%; Score 18; DB 15; Length 9025608;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 TGCTGTCGTACCGTCG 46
DB 7582185 TGCTGTCGTACCGTCG 7582202

RESULT 12
US-10-437-963-97141
; Sequence 97141, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 97141
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(285)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95173C.1
; US-10-437-963-97141

Query Match 32.1%; Score 17; DB 17; Length 285;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GATCCATGACAAATCT 17
DB 255 GATCCATGACAAATCT 271

RESULT 13

US-10-027-632-3534
; Sequence 3534, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3534
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-3534

Query Match 32.1%; Score 17; DB 13; Length 762;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 AAATCTGAATCAACGAG 28
DB 474 AAATCTGAATCAACGAG 490

RESULT 14

```

US-10-027-632-3535
; Sequence 3535, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3535
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-3535

```

```

Query Match      32.1%; Score 17; DB 13; Length 762;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      12 AAATCTGAATCAACCAG 28
      ||||||||||||||||
DB      474 AAATCTGAATCAACCAG 490

```

RESULT 15

```

US-10-027-632-3536
; Sequence 3536, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3536
; LENGTH: 762

```

```

; TYPE: DNA
; ORGANISM: Human
US-10-027-632-3536

```

```

Query Match      32.1%; Score 17; DB 13; Length 762;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      12 AAATCTGAATCAACCAG 28
      ||||||||||||||||
DB      474 AAATCTGAATCAACCAG 490

```

```

Search completed: December 5, 2004, 08:04:09
Job time : 235 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 03:53:58 ; Search time 53 Seconds
(without alignments)
710.789 Million cell updates/sec

Title: US-09-857-841-3
Perfect score: 53
Sequence: 1 gatccatggacaatctgaa.....gtcgtaacccgtcgagagct 53

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	46	86.8	771	3	US-08-875-233-5	Sequence 5, Appli
2	46	86.8	772	3	US-08-875-233-14	Sequence 14, Appl
3	46	86.8	792	3	US-08-875-233-3	Sequence 3, Appli
4	45.8	86.4	130	1	US-08-090-193-14	Sequence 14, Appl
5	45.8	86.4	130	2	US-08-488-031-14	Sequence 14, Appl
6	45.8	86.4	130	2	US-08-486-569-14	Sequence 14, Appl
7	45.8	86.4	130	2	US-08-488-027-14	Sequence 14, Appl
8	45.8	86.4	130	2	US-08-090-192-14	Sequence 14, Appl
9	45.8	86.4	130	2	US-08-482-663-14	Sequence 14, Appl
10	45.8	86.4	130	3	US-08-482-658-14	Sequence 14, Appl
11	45.8	86.4	130	3	US-08-470-349-14	Sequence 14, Appl
12	45.8	86.4	130	3	US-08-475-610-14	Sequence 14, Appl
13	45.8	86.4	130	5	PCT-US92-00277-14	Sequence 14, Appl
14	45.8	86.4	130	5	PCT-US92-00278-14	Sequence 14, Appl
15	45.8	86.4	131	1	US-08-090-193-11	Sequence 11, Appl
16	45.8	86.4	131	2	US-08-488-031-11	Sequence 11, Appl
17	45.8	86.4	131	2	US-08-486-569-11	Sequence 11, Appl
18	45.8	86.4	131	2	US-08-488-027-11	Sequence 11, Appl
19	45.8	86.4	131	2	US-08-090-192-11	Sequence 11, Appl
20	45.8	86.4	131	2	US-08-482-663-11	Sequence 11, Appl
21	45.8	86.4	131	3	US-08-482-658-11	Sequence 11, Appl
22	45.8	86.4	131	3	US-08-470-349-11	Sequence 11, Appl
23	45.8	86.4	131	3	US-08-475-610-11	Sequence 11, Appl
24	45.8	86.4	131	5	PCT-US92-00277-11	Sequence 11, Appl
25	45.8	86.4	131	5	PCT-US92-00278-11	Sequence 11, Appl
26	45.8	86.4	152	1	US-08-090-193-9	Sequence 9, Appli
27	45.8	86.4	152	2	US-08-488-031-9	Sequence 9, Appli

28	45.8	86.4	152	2	US-08-486-569-9	Sequence 9, Appli
29	45.8	86.4	152	2	US-08-488-027-9	Sequence 9, Appli
30	45.8	86.4	152	2	US-08-090-192-9	Sequence 9, Appli
31	45.8	86.4	152	2	US-08-482-663-9	Sequence 9, Appli
32	45.8	86.4	152	3	US-08-482-658-9	Sequence 9, Appli
33	45.8	86.4	152	3	US-08-470-349-9	Sequence 9, Appli
34	45.8	86.4	152	3	US-08-475-610-9	Sequence 9, Appli
35	45.8	86.4	152	5	PCT-US92-00277-9	Sequence 9, Appli
36	45.8	86.4	154	1	US-08-090-193-13	Sequence 13, Appl
37	45.8	86.4	154	2	US-08-488-031-13	Sequence 13, Appl
38	45.8	86.4	154	2	US-08-486-569-13	Sequence 13, Appl
39	45.8	86.4	154	2	US-08-488-027-13	Sequence 13, Appl
40	45.8	86.4	154	2	US-08-090-192-13	Sequence 13, Appl
41	45.8	86.4	154	2	US-08-482-663-13	Sequence 13, Appl
42	45.8	86.4	154	3	US-08-482-658-13	Sequence 13, Appl
43	45.8	86.4	154	3	US-08-470-349-13	Sequence 13, Appl
44	45.8	86.4	154	3	US-08-475-610-13	Sequence 13, Appl
45	45.8	86.4	154	5	PCT-US92-00277-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-875-233-5
Sequence 5, Application US/08875233
Patent No.: 6127601
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26 JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber mosaic virus
STRAIN: V-34
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
OTHER INFORMATION: /codon_start= 3
OTHER INFORMATION: /function= "ENCAPSIDATES VIRUS RNA"

OTHER INFORMATION: /product= "COAT PROTEIN"
OTHER INFORMATION: /gene= "Cp"
OTHER INFORMATION: /number= 1
OTHER INFORMATION: /standard_name= "COAT PROTEIN"
US-08-875-233-5

Query Match 86.8%; Score 46; DB 3; Length 771;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CCATGGACAAATCTGAATCAACCAAGTGTGCTGAACCGTCGACG 49
1 CCATGGACAAATCTGAATCAACCAAGTGTGCTGAACCGTCGACG 46
Db

RESULT 2
US-08-875-233-14
Sequence 14, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: A35
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
US-08-875-233-14

Query Match 86.8%; Score 46; DB 3; Length 772;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CCATGGACAAATCTGAATCAACCAAGTGTGCTGAACCGTCGACG 49
1 CCATGGACAAATCTGAATCAACCAAGTGTGCTGAACCGTCGACG 46
Db

RESULT 3
US-08-875-233-3
Sequence 3, Application US/08875233
Patent No. 6127601

GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: v-33
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
US-08-875-233-3

Query Match 86.8%; Score 46; DB 3; Length 792;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGGACAAATCTGAATCAACCAAGTGTGCTGAACCGTCGACG 49
1 CCATGGACAAATCTGAATCAACCAAGTGTGCTGAACCGTCGACG 46
Db

RESULT 4
US-08-090-193-14
Sequence 14, Application US/08090193
Patent No. 5641673
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5641673bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
;; STREET: 1100 New York Avenue, Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/090,193
;; FILING DATE: 23-DEC-1993
;; CLASSIFICATION: 514
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/00277
;; FILING DATE: 16-JAN-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/642,330
;; FILING DATE: 17-JAN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cimbala, Michele A.
;; REGISTRATION NUMBER: 33,851
;; REFERENCE/DOCKET NUMBER: 0609.3080001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 130 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;;
;; US-08-090-193-14
;;
Query Match 86.4%; Score 45.8; DB 1; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 GATCCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 49
Db 48 GAGTCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 96
;;
RESULT 5
US-08-488-031-14
;; Sequence 14, Application US/08488031
;; Patent No. 5849548
;; GENERAL INFORMATION:
;; APPLICANT: Haseloff, James
;; APPLICANT: Brand, Andrea
;; APPLICANT: Perrimon, No. 5849548bert
;; APPLICANT: Goodman, Howard M.
;; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
;; STREET: 1100 New York Avenue, N.W., Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/488,031
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/090,193
;; FILING DATE: 23-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/00277
;; FILING DATE: 16-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/642,330
;; FILING DATE: 17-JAN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bugalsky, Lawrence B.
;; REGISTRATION NUMBER: 35,086
;; REFERENCE/DOCKET NUMBER: 0609.3080002/MAC/LBB
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 130 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: linear
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;; US-08-488-031-14
;;
Query Match 86.4%; Score 45.8; DB 2; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 GATCCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 49
Db 48 GAGTCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 96
;;
RESULT 6
US-08-486-569-14
;; Sequence 14, Application US/08486569
;; Patent No. 5863774
;; GENERAL INFORMATION:
;; APPLICANT: Haseloff, James
;; APPLICANT: Brand, Andrea
;; APPLICANT: Perrimon, No. 5863774bert
;; APPLICANT: Goodman, Howard M.
;; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
;; STREET: 1100 New York Avenue, N.W., Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,569
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/090,193
;; FILING DATE: 23-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/00277
;; FILING DATE: 16-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/642,330
;; FILING DATE: 17-JAN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bugalsky, Lawrence B.
;; REGISTRATION NUMBER: 35,086
;; REFERENCE/DOCKET NUMBER: 0609.3080006/MAC/LBB
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
US-08-486-569-14

Query Match 86.4%; Score 45.8; DB 2; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GATCCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 49
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Db 48 GAGTCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 96

RESULT 7

US-08-488-027-14
; Sequence 14, Application US/08488027
; Patent No. 5866384
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perimon, No. 5866384bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,027
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/090,193
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3080003/MAC/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
US-08-488-027-14

Query Match 86.4%; Score 45.8; DB 2; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GATCCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 49

Db 48 GAGTCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 96

RESULT 8

US-08-090-192-14
; Sequence 14, Application US/08090192
; Patent No. 5874414
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090,192
; FILING DATE: 11-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/ US 92/00278
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,333
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0609.3030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-090-192-14

Query Match 86.4%; Score 45.8; DB 2; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GATCCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 49
|||
Db 48 GAGTCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 96

RESULT 9

US-08-482-663-14
; Sequence 14, Application US/08482663
; Patent No. 5882907
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perimon, No. 5882907bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,663
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080005/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-482-663-14

Query Match 86.4%; Score 45.8; DB 2; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAATCTGATCAACCACTGCTGCTGTAACCGTCGACG 49
|||
48 GAGTCATGACAATCTGATCAACCACTGCTGCTGTAACCGTCGACG 96

Db

RESULT 10
US-08-482-658-14
Sequence 14, Application US/08482658
Patent No. 6010904
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 6010904bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193

FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080008/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-482-658-14

Query Match 86.4%; Score 45.8; DB 3; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAATCTGATCAACCACTGCTGCTGTAACCGTCGACG 49
|||
48 GAGTCATGACAATCTGATCAACCACTGCTGCTGTAACCGTCGACG 96

Db

RESULT 11
US-08-470-349-14
Sequence 14, Application US/08470349
Patent No. 6015794
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,349
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,192
FILING DATE: 11-NOV-1993
APPLICATION NUMBER: PCT/ US 92/00278
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,333
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-470-349-14

Query Match 86.4%; Score 45.8; DB 3; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GATCCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 48 GAGTCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 12

US-08-475-610-14
Sequence 14, Application US/08475610
Patent No. 6071730

GENERAL INFORMATION:

APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 6071730bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,610
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080004/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-475-610-14

Query Match 86.4%; Score 45.8; DB 3; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GATCCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 48 GAGTCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 13
PCT-US92-00277-14
Sequence 14, Application PC/TUS9200277

GENERAL INFORMATION:

APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, Norbert
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 19920116
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Goldstein, Jorge A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3496604
TELEPHONE: (202) 833-7533
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases

TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPOLOGY: linear

MOLECULE TYPE: DNA
PCT-US92-00277-14

Query Match 86.4%; Score 45.8; DB 5; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GATCCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 48 GAGTCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 14
PCT-US92-00278-14
Sequence 14, Application PC/TUS9200278

GENERAL INFORMATION:

APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00278
FILING DATE: 19920116
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,333
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3476604
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)833-7533
TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Nucleic Acid
PCT-US92-00278-14

Query Match 86.4%; Score 45.8; DB 5; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GATCCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
Db 48 GAGTCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 15

US-08-090-193-11
Sequence 11, Application US/08090193
Patent No. 5641673

GENERAL INFORMATION:

APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5641673bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,193
FILING DATE: 23-DEC-1993
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.

REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-090-193-11

Query Match 86.4%; Score 45.8; DB 1; Length 131;
Best Local Similarity 95.9%; Pred. No. 3.7e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GATCCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
Db 49 GAGTCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 97

Search completed: December 5, 2004, 06:38:56
Job time : 53 secs

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 06:09:28 ; Search time 228 Seconds
(without alignments)
1277.303 Million cell updates/sec

Title: US-09-857-841-3

Perfect score: 53

Sequence: 1 gatccatggacaatctgaa.....gtcgtaacctgcagagct 53

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3694831 seqs, 2747406616 residues

Total number of hits satisfying chosen parameters: 7389662

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	86.8	771	13	US-10-011-033-5
2	46	86.8	772	13	US-10-011-033-14
3	46	86.8	792	13	US-10-011-033-3
4	44.4	83.8	772	13	US-10-011-033-1
5	42.4	80.0	960	13	US-10-011-033-9
6	24.8	46.8	983	13	US-10-011-033-11
7	24	45.3	1068	8	US-08-961-527-373
8	24	45.3	1068	16	US-10-158-844-373
9	23.6	44.5	352	16	US-10-424-599-77125
10	23.2	43.8	1680	15	US-10-369-493-37626
11	22.8	43.0	642	10	US-09-905-666A-20
12	22.8	43.0	766	17	US-10-437-963-47739

US-10-437-963-34792	Sequence 34792, A					
13	22.6	42.6	2718	17	US-10-087-192-37	Sequence 37, Appl
14	22.6	42.6	122859	13	US-09-939-964-1	Sequence 1, Appl
15	22.6	42.3	546	13	US-10-027-632-200344	Sequence 200344,
16	22.4	42.3	546	15	US-10-027-632-200344	Sequence 200344,
17	22.4	42.3	1182	9	US-09-738-626-773	Sequence 773, App
18	22.4	42.3	1266	17	US-10-781-014-619	Sequence 619, App
19	22.4	42.3	3309400	9	US-09-738-626-1	Sequence 1, Appl
20	22.4	41.9	1880	15	US-10-369-493-36410	Sequence 36410, A
21	22.2	41.5	1180	18	US-10-425-115-109275	Sequence 109275,
22	22	41.5	1230	15	US-10-021-723A-7	Sequence 7, Appl
23	22	41.5	3708	10	US-09-758-036-1	Sequence 1, Appl
24	21.8	41.1	1240	17	US-10-767-795-1977	Sequence 1977, Ap
25	21.8	41.1	58320	17	US-10-322-281-88	Sequence 88, Appl
26	21.8	41.1	2256646	17	US-10-470-565-1	Sequence 1, Appl
27	21.6	40.8	255	9	US-09-923-876-1370	Sequence 1370, Ap
28	21.6	40.8	255	10	US-09-923-876-1370	Sequence 1370, Ap
29	21.6	40.8	735	18	US-10-653-047-7425	Sequence 7425, Ap
30	21.6	40.8	1071	16	US-10-425-114-35778	Sequence 35778, A
31	21.6	40.8	1488	18	US-10-818-770-55	Sequence 55, Appl
32	21.6	40.8	1554	16	US-10-425-114-35214	Sequence 9544, Ap
33	21.6	40.8	1554	18	US-10-425-115-9544	Sequence 9553, Ap
34	21.6	40.8	1922	17	US-10-437-963-11860	Sequence 11860, A
35	21.6	40.8	2055	17	US-10-437-963-11860	Sequence 11860, A
36	21.6	40.8	4800	15	US-10-272-291-5	Sequence 5, Appl
37	21.6	40.8	4800	17	US-10-109-048-1141	Sequence 1141, Ap
38	21.6	40.8	4800	17	US-10-628-525-4	Sequence 1630, Ap
39	21.6	40.8	401616	13	US-10-087-192-1630	Sequence 145, App
40	21.4	40.4	473	17	US-10-437-963-145	Sequence 44987, A
41	21.4	40.4	474	18	US-10-425-115-44987	Sequence 69195, A
42	21.4	40.4	746	17	US-10-437-963-69195	Sequence 10976, A
43	21.4	40.4	1309	16	US-10-425-114-10976	Sequence 13947, A
44	21.4	40.4	1386	17	US-10-767-701-13947	
45	21.4	40.4				

ALIGNMENTS

RESULT 1

US-10-011-033-5

Sequence 5, Application US/10011033

Publication No. US20020124286A1

GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J

TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber mosaic virus
STRAIN: V-34
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
OTHER INFORMATION: /codon_start= 3
/function= "ENCAPSIDATES VIRUS RNA"
/product= "COAT PROTEIN"
/gene= "CP"
/number= 1
/standard_name= "COAT PROTEIN"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-011-033-5

Query Match 86.8%; Score 46; DB 13; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
Db 1 CCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46

RESULT 2
US-10-011-033-14
Sequence 14, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: A35
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-011-033-14

Query Match 86.8%; Score 46; DB 13; Length 772;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
Db 1 CCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46

RESULT 3
US-10-011-033-3
Sequence 3, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS

STRAIN: v-33
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-011-033-3

Query Match 86.8%; Score 46; DB 13; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 49
1 CCATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 46
Db

RESULT 4
US-10-011-033-1

Sequence 1, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J

TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.

STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,033

FILING DATE: 13-No. US20020124286A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/875,233

FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lisa V. Mueller

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 772 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Cucumber Mosaic Virus

INDIVIDUAL ISOLATE: V-27

FEATURE:

NAME/KEY: CDS

LOCATION: 3..660

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-011-033-1

Query Match 83.8%; Score 44.4; DB 13; Length 772;
Best Local Similarity 97.8%; Pred. No. 6.8e-08;

Matches 45; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 CCATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 49
1 CCATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCGCG 46
Db

RESULT 5
US-10-011-033-9

Sequence 9, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J

TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.

STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,033

FILING DATE: 13-No. US20020124286A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/875,233

FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lisa V. Mueller

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 960 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: CUCUMBER MOSAIC VIRUS

STRAIN: STRAIN C

FEATURE:

NAME/KEY: CDS

LOCATION: 1..658

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-011-033-9

Query Match 80.0%; Score 42.4; DB 13; Length 960;
Best Local Similarity 97.7%; Pred. No. 4.8e-07;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 49
1 ATGACAATCTGAATCAACCAAGTGTGTCGTAACCATCGACG 44
Db

RESULT 6
US-10-011-033-11

GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Steetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
JOURNAL: J. Gen. Virol.
VOLUME: 70
PAGES: 1065-1073
DATE: 1989
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-011-033-11
Query Match 46.8%; Score 24.8; DB 13; Length 983;
Best Local Similarity 72.7%; Pred. No. 7.8;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 6 ATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
Db 1 ATGACAAATCTGATCTCCCAATGCTAGTAGAACCTCCCGCG 44
RESULT 7
US-08-961-527-373
Sequence 373, Application US/08961527
Publication No. US20020032323A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 373:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-373

Query Match 45.3%; Score 24; DB 8; Length 1068;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 13 AATCTGAATCAACCAAGTGTGCTGTAACCGTCGACGACC 52
Db 150 AATCTGATCAACCAAGTGTGCTCACTCAGCATCGACACAGC 189

RESULT 8
US-10-158-844-373
Sequence 373, Application US/10158844
Publication No. US20040029118A1
GENERAL INFORMATION:
APPLICANT: Kunsch et al.
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude Pentium 3
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/158,844
FILING DATE: 03-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/961,527
FILING DATE: 1997-10-30
APPLICATION NUMBER: US 60/029,960
FILING DATE: 1996-10-31
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB340P1D1
INFORMATION FOR SEQ ID NO: 373:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 373:
US-10-158-844-373

Query Match 45.3%; Score 24; DB 16; Length 1068;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 34792
LENGTH: 2718
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_38773C.1
US-10-437-963-34792

Query Match 42.6%; Score 22.6; DB 17; Length 2718;
Best Local Similarity 75.7%; Pred. No. 80;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 CTGAATCAACAGTGTGCTGTAACCGTCGACGAGC 52
DB 519 CTGAACATGCGCGCTGGCAGTAACCGAGACGAGC 483

RESULT 14
US-10-087-192-37/C
Sequence 37, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 122859
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(122859)
OTHER INFORMATION: n = A,T,C or G
US-10-087-192-37

Query Match 42.6%; Score 22.6; DB 13; Length 122859;
Best Local Similarity 75.7%; Pred. No. 2.1e+02;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 ATCCATGACAAATCTGAATCAACCACTGCTGCTGT 38
DB 9102 AGCCTTGACAAATCTTAATGACGATTGTGAGGT 9066

RESULT 15
US-09-939-964-1
Sequence 1, Application US/09939964
Publication No. US20030054522A1
GENERAL INFORMATION:
APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph

APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
FILE REFERENCE: CARP0068
CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 536165
TYPE: DNA
ORGANISM: Rhizobium
US-09-939-964-1

Query Match 42.6%; Score 22.6; DB 10; Length 536165;
Best Local Similarity 68.9%; Pred. No. 3e+02;
Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 9 GACAAATCTGAATCAACCACTGCTGCTGAACCGTCGACGAGCT 53
DB 525007 GACGAACGTGATCATGACGTGCTGATCGCAACGCTCGACCGGCT 525051

Search completed: December 5, 2004, 07:06:42
Job time : 232 secs

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 06:13:23 ; Search time 221 Seconds
(without alignments)
1258.911 Million cell updates/sec

Title: US-09-857-841-3

Perfect score: 53
Sequence: 1 gatccatgacaatctgaa.....gtcgtaccgtcgacgagct 53

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	53	100.0	53	3	AAA30858	Aaa30858 Ubiquitin
2	46	86.8	771	2	AAT34666	Aat34666 Coat prot
3	46	86.8	773	2	AAT34665	Aat34665 Coat prot
4	45	84.9	976	2	AAQ10461	Aaq10461 Capsid pr
5	45	84.9	1007	2	AAQ10462	Aaq10462 Capsid pr
6	45	84.9	1007	2	AAQ67395	Aaq67395 Cauliflow
7	45	84.9	1066	2	AAT9545	Aat9545 Cucumber
8	45	84.9	1067	2	AAZ07505	Aaz07505 Cucumber
9	45	84.9	1379	1	AAN81111	Aan81111 Sequence
10	45	84.9	1696	2	AAQ76107	Aaq76107 Cucumber
11	45	84.9	1860	2	AAQ76106	Aaq76106 Cucumber
12	45	84.9	2173	2	AAQ76108	Aaq76108 Cucumber
13	43	81.1	772	2	AAT34664	Aat34664 Coat prot
14	43	81.1	772	2	AAT17259	Aat17259 Coat prot
15	38	71.7	894	3	ABL58209	Ab158209 Agrobacte
16	38	71.7	1423	1	AAN90249	Aan90249 Cucumber
17	38	71.7	1426	2	AAT72272	Aat72272 Cucumber
18	37	69.8	657	2	AAQ03641	Aaq03641 Cucumber
19	20	37.7	25	2	AAQ00796	Aax00796 Primer YR
20	17	32.1	20	2	AAQ80688	Aaq80688 CMV-SA cd
21	17	32.1	639	3	AA64858	Aa64858 Bordetell

22	17	32.1	657	2	AAQ41742	Aaq41742 Cucumber
23	17	32.1	657	2	AAQ80683	Aaq80683 CMV-SA co
24	17	32.1	1128	3	AAQ45252	Aac45252 Arabidops
25	17	32.1	1132	3	AAQ36474	Aac36474 Arabidops
26	17	32.1	28854	8	ABX95685	Abx95685 Human gen
27	17	32.1	35026	3	AAA64890	Aaa64890 Bordetell
28	17	32.1	334462	10	ADC24763	Adc24763 Human wil
29	16	30.2	35	2	AAQ92815	Aaq92815 DNA prime
30	16	30.2	35	2	AAT38246	Aat38246 Y. pestis
31	16	30.2	542	4	AAQ43396	Aa43396 DNA encod
32	16	30.2	542	4	AAI93810	Aai93810 Human pol
33	16	30.2	639	3	AAZ45575	Aaz45575 Nucleotid
34	16	30.2	762	4	ABL09345	Ab109345 Drosophil
35	16	30.2	3118	4	ABL09344	Ab109344 Drosophil
36	16	30.2	4116	6	ABK24522	Abk24522 EIF-2alph
37	16	30.2	11463	2	AAQ34650	Aax34650 Starch br
38	16	30.2	11475	5	AAH78338	Aah78338 Nucleotid
39	16	30.2	11476	12	ADF89961	Adf89961 A. tausch
40	16	30.2	13500	3	AAZ45562	Aaz45562 Nucleotid
41	16	30.2	335199	10	ADC24703	Adc24703 Human wil
42	15	28.3	99	12	ADG93176	Adg93176 Novel exp
43	15	28.3	99	12	ADG93175	Adg93175 Novel exp
44	15	28.3	99	12	ADJ65853	Adj65853 GLP-2 pep
45	15	28.3	99	12	ADJ65854	Adj65854 GLP-2 pep

ALIGNMENTS

RESULT 1	AAA30858	standard; DNA; 53 BP.
ID	AAA30858	
XX	AAA30858;	
AC	19-SEP-2000	(first entry)
DT	Ubiquitin monomer C-terminal fragment coding sequence.	
DE	Ubiquitin monomer; protein production; plant cell; ubiquitin promoter;	
XX	ds.	
KW	Nicotiana tabacum.	
XX		
OS		
XX		
FH	Key	Location/Qualifiers
FT	CDS	6..47
FT		/*tag= a
FT		/product= "Ubiquitin_monomer_fragment"
FT		/partial
XX		
PN	WO200036129-A1.	
XX		
PD	22-JUN-2000.	
XX		
PF	11-DEC-1998;	98WO-SG000103.
XX		
PR	11-DEC-1998;	98WO-SG000103.
XX		
PA	(MOLE-) INST MOLECULAR AGROBIOLOGY.	
XX		
PI	Fang R, Wu J, Chen X;	
XX		
DR	WPI; 2000-431604/37.	
DR	P-PSDB; AAY90255.	
XX		
XX	Production of desired protein in plants or plant cells by linking a	
PT	ubiquitin monomer coding sequence upstream of the gene encoding the	
PT	desired protein.	
XX		
PS	Claim 8; Page 18; 42pp; English.	
XX		
CC	This sequence encodes the C-terminal fragment of a ubiquitin monomer. The	
CC	invention relates to a method for enhancing production of a desired	

CC protein in a plant or plant cell by inserting a nucleic acid (NA)
CC encoding a ubiquitin monomer upstream of a NA encoding the desired
CC protein, where the fusion construct encodes a fusion protein and
CC expression is not controlled by the ubiquitin promoter. The invention
CC also relates to a NA acid vector a NA vector able to transform a plant
CC cell, that comprises NA encoding a fusion protein having a ubiquitin
CC monomer linked to a protein of interest and further, where expression of
CC the fusion construct is not under control of a ubiquitin promoter. The
CC construct allows enhanced production of the desired protein in plants or
CC plant cells
XX
SQ Sequence 53 BP; 15 A; 14 C; 13 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 53; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 6.1e-19;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATCCATGACAAATCTGAATCAACAGTGTGTCGTAACCGTCGACGAGCT 53
|||
Db 1 GATCCATGACAAATCTGAATCAACAGTGTGTCGTAACCGTCGACGAGCT 53

RESULT 2
AAT34666
ID AAT34666 standard; DNA; 771 BP.
XX
AC AAT34666;

XX 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)

XX Coat protein of the V34 strain of cucumber mosaic virus.

XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KW resistance; ss.

XX Cucumber mosaic virus; strain V34.

XX Key location/Qualifiers
FT CDS 3..659
FT /*tag= a

PN WO9621018-A1.

XX 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

XX WPI; 1996-333993/33.

XX P-PSDB; AAR98895.

XX New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.

XX Claim 24; Fig 3; 80pp; English.

XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 771 BP; 176 A; 199 C; 183 G; 213 T; 0 U; 0 Other;

Query Match 86.8%; Score 46; DB 2; Length 771;

Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCATGACAAATCTGAATCAACAGTGTGTCGTAACCGTCGACG 49
|||
Db 1 CCATGACAAATCTGAATCAACAGTGTGTCGTAACCGTCGACG 46

RESULT 3
AAT34665
ID AAT34665 standard; DNA; 773 BP.
XX
AC AAT34665;

XX 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)

XX Coat protein of the V33 strain of cucumber mosaic virus.

XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KW resistance; ss.

XX Cucumber mosaic virus; strain V33.

XX Key location/Qualifiers
FT CDS 3..659
FT /*tag= a

PN WO9621018-A1.

XX 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

XX WPI; 1996-333993/33.

XX P-PSDB; AAR98894.

XX New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.

XX Claim 13; Fig 2; 80pp; English.

XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 773 BP; 175 A; 200 C; 185 G; 213 T; 0 U; 0 Other;

Query Match 86.8%; Score 46; DB 2; Length 773;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCATGACAAATCTGAATCAACAGTGTGTCGTAACCGTCGACG 49
|||
Db 1 CCATGACAAATCTGAATCAACAGTGTGTCGTAACCGTCGACG 46

RESULT 4
AAQ10461
ID AAQ10461 standard; cDNA; 976 BP.

XX AAQ10461;

DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-APR-1991 (first entry)
XX
XX Capsid protein gene of Cucumber Mosaic Virus strain FNY.
XX
XX CMV; resistance; capsid protein; Cucumis melo; ss.
XX
XX Cucumber mosaic virus.
XX
XX
XX Key Location/Qualifiers
FT CDS 75..731
FT /*tag= a
FT /product= "CMV strain FNY capsid protein"
XX
XX EP412912-A.
XX
XX 13-FEB-1991.
XX
XX 09-AUG-1990; 90EP-00402282.
XX
XX 11-AUG-1989; 89FR-00010848.
XX
XX (BIOC-) BIOCEM SA.
XX
XX Deboth M, Bentahar S, Noel M, Perret J;
XX
XX WPI; 1991-046027/07.
DR P-PSDB; AAR10652.
XX
XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
PT culture on specific medium for new transformed plants etc., esp.
PT resistant to cucumber mosaic virus.
XX
XX Claim 15; Page 17; 44pp; French.
XX
XX The gene was isolated from a plasmid (pUC18) containing DNA complementary
CC to RNA 3 of the virulent strain FNY, isolated in New York on infected
CC melons. The sequence includes a leader sequence, coding region and 3' non
CC -coding region. The leader sequence is the same length as that of the
CC Japanese Y strain of CMV. Transgenic melon plantlets containing the
CC sequence introduced via an Agrobacterium tumefaciens intermediate are
CC cultured as shoots in special media. The transformed melon plants are
CC resistant to CMV. See also AAQ10462. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC AUG-2003 to correct OS field.)
XX
XX Sequence 976 BP; 224 A; 249 C; 230 G; 273 T; 0 U; 0 Other;
SQ
Query Match 84.9%; Score 45; DB 2; Length 976;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 74 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 118
RESULT 5
AAQ10462
ID AAQ10462 standard; DNA; 1007 BP.
XX
XX AAQ10462;
XX
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-APR-1991 (first entry)
XX
XX Capsid protein gene of Cucumber Mosaic Virus strain 117F.
XX
XX CMV; resistance; capsid protein; Cucumis melo; ss.
XX
XX Cucumber mosaic virus.
OS

XX
XX Key Location/Qualifiers
FH CDS 54..710
FT /*tag= a
FT /product= "CMV strain 117F capsid protein"
XX
XX EP412912-A.
XX
XX 13-FEB-1991.
XX
XX 09-AUG-1990; 90EP-00402282.
XX
XX 11-AUG-1989; 89FR-00010848.
XX
XX (BIOC-) BIOCEM SA.
XX
XX Deboth M, Bentahar S, Noel M, Perret J;
XX
XX WPI; 1991-046027/07.
DR P-PSDB; AAR10653.
XX
XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
PT culture on specific medium for new transformed plants etc., esp.
PT resistant to cucumber mosaic virus.
XX
XX Claim 16; Page 19; 44pp; French.
XX
XX The gene was isolated from the virulent French strain 117F of CMV. Tomato
CC plantlets at the 2-leaf stage were infected with CMV strain 117F. 15 days
CC post-infection, the virus was purified from the infected leaves and cDNA
CC was synthesised from RNAs 1,2,3 and 4. After purification and selection
CC by standard techniques, cDNA complementary to RNA 4 was found to encode
CC the capsid protein. It was recloned into "Blue scribe" plasmids and
CC sequenced. Transgenic melon plantlets containing the sequence introduced
CC via an Agrobacterium tumefaciens intermediate are cultured as shoots in
CC special media. The transformed melon plants are resistant to CMV. See
CC also AAQ10461. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
CC 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
CC field.)
XX
XX Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;
SQ
Query Match 84.9%; Score 45; DB 2; Length 1007;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 53 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 97
RESULT 6
AAQ67395
ID AAQ67395 standard; DNA; 1007 BP.
XX
XX AAQ67395;
XX
XX 25-MAR-2003 (revised)
DT 12-APR-1995 (first entry)
XX
XX Cauliflower mosaic virus capsid protein coding sequence.
XX
XX Cauliflower mosaic virus; CMV; capsid protein; coat protein;
KW polyribozyme; inactivate; inactivation; resistance; crop protection; ss.
XX
XX Cauliflower mosaic virus.
XX
XX Key Location/Qualifiers
FH CDS 54..710
FT /*tag= a
FT /product= "Capsid protein."
XX
XX FR2701960-A1.
PN

```
XX 02-SEP-1994.
PD
XX 26-FEB-1993; 93FR-00002269.
PF
XX 26-FEB-1993; 93FR-00002269.
PR
XX (GENE-) GENE SHEARS PTY LTD.
PA
XX Lenee P, Perez P, Gruber V, Baudot G, Ollivo C;
PI
XX WPI; 1994-281767/35.
XX P-PSDB; AAR57968.
DR
XX
XX New polyribozyme contg. several catalytic regions in complementary
PT sequence - can inactivate gene for viral capsid protein, esp. for prepn.
PT of new virus resistant transgenic plants, also DNA sequence encoding it.
XX
XX Disclosure; Fig 2; 67pp; French.
PS
XX The RNA encoding the capsid protein of cauliflower mosaic virus can be
CC targeted by a nucleic acid sequence called a "polyribozyme". The
CC polyribozyme has endoribonuclease activity and is able to inactivate the
CC gene encoding the viral capsid protein. The polyribozyme comprises
CC several catalytic regions derived from ribozymes and confers complete
CC resistance to virus. See AAQ67391-94. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;
Query Match 84.9%; Score 45; DB 2; Length 1007;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CATGACAATCTGATCAACCACTGCTGCTGTAACCGTCGACG 49
Db 53 CATGACAATCTGATCAACCACTGCTGCTGTAACCGTCGACG 97
RESULT 7
AAT99545/c
ID AAT99545 standard; cDNA; 1066 BP.
XX
AC AAT99545;
XX
DT 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
DE Cucumber mosaic virus RNA-3 cDNA fragment.
XX
KM Transgenic plant; virus resistance; disease resistance; RNA virus; CMV;
KM coat protein; antisense gene; ss.
XX
OS Cucumber mosaic virus.
XX
XX Key Location/Qualifiers
FH 3'UTR 1..299
FT /*tag= a
FT CDS 300..958
FT /*tag= b
FT /*product= "coat protein"
FT sig_peptide 956..1029
FT /*tag= c
FT /*note= "coat protein leader sequence"
FT promoter 1030..1066
FT /*tag= d
FT /*note= "F sequence of sub-genomic promoter"
XX
XX EP806481-A2.
XX
XX 12-NOV-1997.
XX
XX 07-MAY-1997; 97EP-00201379.
XX
```

```
XX 09-MAY-1996; 96IT-MI000927.
PR
XX (META-) METAPONTUM AGROBIOS SCRL.
XX
XX Cellini F, Grieco PD;
PI
XX WPI; 1997-538620/50.
DR
XX
XX Preparing transgenic plants resistant to RNA virus infection - using
PT anti:sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
XX Claim 3; Page 10; 18pp; English.
PS
XX This cDNA clone of cucumber mosaic virus (CMV) RNA-3 includes domain F of
CC the subgenomic promoter of viral RNA, the coat protein gene, its leader
CC sequence, and the tRNA-like 3'-terminal region of RNA-3. It was prepared
CC by amplifying a fragment of CMV cDNA-3 from clone PCR-CMV1RNA3 by PCR
CC (see also AAT99548-49). The gene construct is introduced into a vector
CC containing a promoter active in plant cells in antisense orientation
CC relative to the promoter. A claimed recombinant vector comprises the
CC plant promoter, the antisense gene construct and a terminator which is
CC functional in the plant. In addition to CMV, viral RNA may also be used
CC from tobacco mosaic virus and potato virus. Claimed transgenic plants
CC have the antisense gene construct integrated into their genomes. They are
CC resistant to viral infection. In particular, they are resistant to CMV.
CC Within the antisense gene construct, the interfering activity of the
CC antisense F domain of the sub-genomic promoter, associated with the
CC antisense activity performed by the coat protein gene, allows production
CC of plants having 100% resistance to CMV. (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 1066 BP; 299 A; 251 C; 273 G; 243 T; 0 U; 0 Other;
Query Match 84.9%; Score 45; DB 2; Length 1066;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CATGACAATCTGATCAACCACTGCTGCTGTAACCGTCGACG 49
Db 957 CATGACAATCTGATCAACCACTGCTGCTGTAACCGTCGACG 913
RESULT 8
AAZ07505/c
ID AAZ07505 standard; cDNA; 1067 BP.
XX
AC AAZ07505;
XX
DT 26-NOV-1999 (first entry)
DT
XX
DE Cucumber mosaic virus (CMV) RNA-3 gene cDNA clone fragment.
XX
KM Transgenic plant; RNA virus; antisense construct; cucumber mosaic virus;
KM CMV; promoter; coat protein gene; infection; RNA-3; ss.
XX
OS Cucumber mosaic virus.
XX
XX US5959181-A.
XX
XX 28-SEP-1999.
XX
XX 09-MAY-1997; 97US-00854170.
XX
XX 09-MAY-1996; 96IT-MI000927.
XX
XX (META-) METAPONTUM AGROBIOS SCRL.
XX
XX Cellini F, Grieco PD;
PI
XX WPI; 1997-538620/50.
XX
XX
```


PT Preparing transgenic plants resistant to RNA virus infection - using
PT anti:sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
PS Claim 2; Fig 1; 15pp; English.
XX
CC The invention relates to preparing transgenic plants resistant to RNA
CC virus induced infections that comprises integrating an antisense gene
CC construct into the plant genome. The construct comprises: (a) an F domain
CC of a subgenomic promoter of cucumber mosaic virus (CMV); (b) downstream
CC from the subgenomic promoter, a leader sequence of a coat protein gene of
CC CMV; (c) downstream from the leader sequence, a gene encoding a CMV coat
CC protein; and (d) downstream from the gene, a 3'-terminal region of a CMV
CC coat protein gene. The method is useful for producing plants which are
CC resistant to infection by RNA based viruses. The gene construct gives
CC higher levels of resistance compared to antisense constructs which are
CC capable of complementing with different domains of genomic RNA of CMV.
CC The present sequence represents the fragment of cDNA clone of RNA-3 of
CC CMV. This forms the antisense construct of the invention
XX
SQ Sequence 1067 BP; 297 A; 250 C; 276 G; 244 T; 0 U; 0 Other;
XX
Query Match 84.9%; Score 45; DB 2; Length 1067;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
Db CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 913
XX
RESULT 9
AAN81111
ID AAN81111 standard; DNA; 1379 BP.
XX
AC AAN81111;
XX
DT 25-MAR-2003 (revised)
DT 12-NOV-1990 (first entry)
XX
XX Sequence contg. CMV strain Y coat protein gene.
DE
XX Cucurber mosaic virus; plant viral resistance; ss.
KW
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT CDS 418..1074
FT /*tag= a
FT /label= cucumber mosaic virus-Y coat protein.
XX
XX EP279433-A.
PN
XX
XX 24-AUG-1988.
PD
XX
XX 18-FEB-1988; 88EP-00102322.
PF
XX
PR 20-FEB-1987; 87JP-00038288.
PR 25-FEB-1987; 87JP-00043443.
PR 18-FEB-1988; 88JP-00035809.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
PA
XX
PI Furusawa I, Onda H, Komiya T;
XX
XX WPI; 1988-236708/34.
DR
DR P-PSDB; AAP80509.
XX
XX DNA coding for the coat protein of cucumber mosaic virus strain Y - used
PT for producing plants resistant to cucumber mosaic virus infection.
XX
PS Disclosure; Page ?; 20pp; English.
XX

CC This DNA is produced on screening of a plasmid library and is used to
CC transform plant cells which subsequently produce the coat prot- ein of
CC cucumber mosaic virus (CMV) strain Y. This protein is not synthesised in
CC natural plant cells. The resistance to CMV infect- ion, provided by the
CC DNA, is shown in plant cells and redifferent- iated plant bodies. See
CC also AAN81110. (Updated on 25-MAR-2003 to correct PR field.) (Updated on
CC 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1379 BP; 306 A; 342 C; 333 G; 398 T; 0 U; 0 Other;
XX
Query Match 84.9%; Score 45; DB 1; Length 1379;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
Db CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 461
XX
RESULT 10
AAQ76107
ID AAQ76107 standard; DNA; 1696 BP.
XX
XX AAQ76107;
AC
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
XX Cucurber mosaic virus RNA-3 chimera encoding RNase T1.
DE
XX
KW Cucurber mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; RNase T1;
KW cell inhibitory protein; ToMV; CMV; ss.
XX
XX Cucurber mosaic virus.
OS
XX
XX
FH Key Location/Qualifiers
FT CDS 123..437
FT /*tag= a
FT /product= "RNase T1"
FT
XX
XX WO9429464-A1.
PN
XX
XX 22-DEC-1994.
PD
XX
XX 03-JUN-1994; 94WO-EP001817.
PF
XX
PR 04-JUN-1993; 93GB-00011593.
XX
XX (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GBS MBH.
XX
PI De Haan PT;
XX
XX WPI; 1995-036490/05.
DR
DR P-PSDB; AAR67754.
XX
XX DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.
XX
XX Claim 4; Page 31-32; 50pp; English.
PS
XX
XX A chimeric cucumber mosaic virus RNA-3 (given in AAQ76107) has the coat
CC protein gene replaced by a gene encoding a cell inhibitory protein, RNase
CC T1, having the sequence given in AAR67754. The construct elicits a minus-
CC sense RNA that interacts with the RNA-dependent RNA-polymerase of an
CC invading virus, thus conferring virus-resistance on a host plant, e.g.
CC tobacco, tomato. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 1696 BP; 387 A; 413 C; 389 G; 507 T; 0 U; 0 Other;
Query Match 84.9%; Score 45; DB 2; Length 1696;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
DB 732 CATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 776

RESULT 11
AAQ76106
ID AAQ76106 standard; DNA; 1860 BP.

XX AAQ76106;

DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)

DE Cucumber mosaic virus RNA-3 chimera encoding TOMV CP.

KW Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; coat protein; CP;
KM TOMV; CMV; 88.

XX OS Cucumber mosaic virus.

XX Key Location/Qualifiers
FH CDS 123..600
FT /*tag= a

FT /product= "TOMV coat protein"
FT 895..1550
FT /*tag= b
FT /product= "CMV coat protein"

XX PN WO9429464-A1.

XX PD 22-DEC-1994.

XX PF 03-JUN-1994; 94WO-EP001817.

XX PR 04-JUN-1993; 93GB-00011593.

XX PA (SANO) SANDOZ LTD.

XX PA (SANO) SANDOZ PATENT GMBH.

XX PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX PI De Haan PT;

XX PS WPI; 1995-036490/05.

XX DR P-PSDB; AAR67752, AAR67753.

XX PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.

XX PS Claim 3; Page 27-28; 50pp; English.

XX CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76106) codes for the
CC coat protein (CP) of tomato mosaic virus (AAR67752) as well as its own CP
CC (AAR67753). The construct elicits minus-sense RNA that interacts with the
CC RNA-dependent RNA-polymerase of an invading virus, thus conferring virus-
CC resistance on a host plant, e.g. tobacco, tomato. (Updated on 25-MAR-2003
CC to correct PN field.)

XX SQ Sequence 1860 BP; 448 A; 429 C; 431 G; 552 T; 0 U; 0 Other;

Query Match 84.9%; Score 45; DB 2; Length 1860;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
DB 896 CATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 940

RESULT 12
AAQ76108
ID AAQ76108 standard; DNA; 2173 BP.

XX AAQ76108;

DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)

DE Cucumber mosaic virus RNA-3 chimera encoding TOMV P30.

KW Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; P30; elicitor; TOMV;
KM CMV; 88.

XX OS Cucumber mosaic virus.

XX Key Location/Qualifiers
FH CDS 123..914
FT /*tag= a
FT /product= "TOMV P30 elicitor"

XX PN WO9429464-A1.

XX PD 22-DEC-1994.

XX PF 03-JUN-1994; 94WO-EP001817.

XX PR 04-JUN-1993; 93GB-00011593.

XX PA (SANO) SANDOZ LTD.

XX PA (SANO) SANDOZ PATENT GMBH.

XX PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX PI De Haan PT;

XX PS WPI; 1995-036490/05.

XX DR P-PSDB; AAR67755.

XX PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.

XX PS Claim 5; Page 34-35; 50pp; English.

XX CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76108) has the coat
CC protein gene replaced by a gene encoding an elicitor, TOMV P30, having
CC the sequence given in AAR67755. The construct elicits a minus-sense RNA
CC that interacts with the RNA-dependent RNA-polymerase of an invading
CC virus, thus conferring virus-resistance on a host plant, e.g. tobacco,
CC tomato. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 2173 BP; 561 A; 438 C; 532 G; 642 T; 0 U; 0 Other;

Query Match 84.9%; Score 45; DB 2; Length 2173;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||||
DB 1209 CATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 1253

RESULT 13
AAT34664

```
ID AAT34664 standard; DNA; 772 BP.
XX
AC AAT34664;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the V27 strain of cucumber mosaic virus.
XX
KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance; ss.
XX
OS Cucumber mosaic virus; strain V27.
XX
FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a
XX
PN WO9621018-A1.
XX
PD 11-JUL-1996.
XX
PF 07-JUN-1995; 95WO-US007234.
XX
PR 30-DEC-1994; 94US-00367789.
XX
PA (ASGR-) ASGROW SEED CO.
XX
PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
DR WPI; 1996-333993/33.
XX
DR P-PSDB; AAR98893.
XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
PS Claim 2, Fig 1; 80pp; English.
XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 772 BP; 177 A; 202 C; 182 G; 211 T; 0 U; 0 Other;

Query Match 81.1%; Score 43; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCG 46
Db 1 CCATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCG 43

RESULT 14
AAT17259
ID AAT17259 standard; DNA; 772 BP.
XX
AC AAT17259;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the A35 strain of cucumber mosaic virus.
XX
KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance; ss.
XX
OS Cucumber mosaic virus; strain A35.
XX
```

```
FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a
XX
PN WO9621018-A1.
XX
PD 11-JUL-1996.
XX
PF 07-JUN-1995; 95WO-US007234.
XX
PR 30-DEC-1994; 94US-00367789.
XX
PA (ASGR-) ASGROW SEED CO.
XX
PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
DR WPI; 1996-333993/33.
DR P-PSDB; AAR93803.
XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
PS Disclosure; Fig 8; 80pp; English.
XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 772 BP; 175 A; 201 C; 185 G; 211 T; 0 U; 0 Other;

Query Match 81.1%; Score 43; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCG 46
Db 1 CCATGACAATCTGAATCAACCAAGTGTGTCGTAACCGTCG 43

RESULT 15
ABL58209
ID ABL58209 standard; DNA; 894 BP.
XX
AC ABL58209;
XX
DT 25-JUL-2002 (first entry)
XX
DE Agrobacterium tumefaciens coding sequence.
XX
KW Agrobacterium tumefaciens; anti-cucumber mosaic virus; transgenic tomato;
KM ss.
XX
OS Agrobacterium tumefaciens.
XX
FH Key Location/Qualifiers
FT CDS 105..760
FT /*tag= a
FT /product= "Agrobacterium tumefaciens protein"
XX
PN KR99075101-A.
XX
PD 05-OCT-1999.
XX
PF 17-MAR-1998; 98KR-00009096.
XX
PR 17-MAR-1998; 98KR-00009096.
XX
PA (RURA-) RURAL DEV ADMINISTRATION.
XX
```

PI Sohn SH, Lee SW, Park JS, Hwang YS;
XX
DR WPI; 2000-577926/54.
DR P-PSDB; ABB80503.
XX
PT Anti-cucumber mosaic virus tomato.
XX
PS Disclosure; Page 4; 6pp; Korean.
XX
CC This sequence represents a coding sequence from Agrobacterium tumefaciens
CC used within the scope of the invention. The invention relates to an anti-
CC cucumber mosaic virus tomato
XX
SQ Sequence 894 BP; 188 A; 228 C; 216 G; 262 T; 0 U; 0 Other;

Query Match 71.7%; Score 38; DB 3; Length 894;
Best Local Similarity 100.0%; Pred. No. 7.6e-11;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AAATCTGAATCAACCAAGTGTGTGCTAACCCTGACG 49
Db 111 AAATCTGAATCAACCAAGTGTGTGCTAACCCTGACG 148

Search completed: December 5, 2004, 07:10:27
Job time : 223 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2004, 07:10:32 ; Search time 71 Seconds
(without alignments)
70.735 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSGRNRR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqp19908:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20048:*

8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	14	3	AAY90255 Ubiquitin
2	69	100.0	218	2	AAR10652 Capsid pr
3	69	100.0	218	2	AAR10653 Capsid pr
4	69	100.0	218	2	AAR57968 Cauliflow
5	69	100.0	218	2	AAR67753 CMV coat
6	69	100.0	218	2	AAR93803 Coat prot
7	69	100.0	218	2	AAR98893 Coat prot
8	69	100.0	218	2	AAR98894 Coat prot
9	69	100.0	218	2	AAR98895 Coat prot
10	61	88.4	218	3	ABR80503 Agrobacte
11	44	63.8	438	8	AD061973 Transcrip
12	42	60.9	218	2	AAR37212 Cucumbe
13	40	58.0	289	3	AAG05253 Arabidops
14	39	56.5	64	3	AAG00746 Human sec
15	39	56.5	68	8	ABO57865 Human gen
16	39	56.5	261	6	AAR36184 Human CGD
17	39	56.5	271	4	AAM41266 Human pol
18	39	56.5	274	4	AAM23534 Novel hum
19	39	56.5	280	6	ABU11773 Human MDD
20	39	56.5	287	4	AAM39480 Human pol
21	39	56.5	407	4	ABR61652 Drosophil
22	39	56.5	1046	7	AD58906 Human Pro
23	39	56.5	1046	7	ADD45534 Human Pro
24	39	56.5	1046	7	AD61258 Human Pro
25	39	56.5	1046	7	AD58902 Human Pro

26	38	55.1	54	4	AAU41552 Propionib
27	38	55.1	54	6	ABM38071 Propionib
28	38	55.1	197	8	ADO57439 Hairless
29	38	55.1	372	2	AAR22239 Human ZP3
30	38	55.1	372	3	AAY67287 Human zon
31	38	55.1	530	7	ADC07876 Rice prot
32	38	55.1	530	7	ADC08287 Rice prot
33	38	55.1	562	8	ADP43232 Nematode
34	38	55.1	624	8	ADP43243 Nematode
35	38	55.1	626	8	ADP43242 Nematode
36	38	55.1	1511	2	AAY32080 Yeast wea
37	38	55.1	1517	3	AAG38482 Arabidops
38	38	55.1	1543	3	AAG38481 Arabidops
39	38	55.1	1672	3	AAG38480 Arabidops
40	38	55.1	19938	6	ABP76680 Streptomy
41	37	53.6	69	5	ABP03145 Human ORF
42	37	53.6	86	3	AAG26614 Arabidops
43	37	53.6	95	4	AAG6349 Propionib
44	37	53.6	95	4	AAG64628 Propionib
45	37	53.6	95	6	ABM61147 Propionib

ALIGNMENTS

RESULT 1	
AAAY90255	standard; protein; 14 AA.
ID	AAAY90255 standard; protein; 14 AA.
XX	
AC	AAAY90255;
DT	19-SEP-2000 (first entry)
XX	
DE	Ubiquitin monomer C-terminal fragment.
XX	
KW	Ubiquitin monomer; protein production; plant cell; ubiquitin promoter.
XX	
OS	Nicotiana tabacum.
XX	
PN	WO200036129-A1.
XX	
PD	22-JUN-2000.
XX	
PF	11-DEC-1998; 98WO-SG000103.
XX	
PR	11-DEC-1998; 98WO-SG000103.
XX	
PA	(MOLE-) INST MOLECULAR AGROBIOLOGY.
XX	
PI	Fang R, Wu J, Chen X;
XX	
DR	WPI; 2000-431604/37.
XX	
PS	N-PSDB; AAA30858.
XX	
PT	Production of desired protein in plants or plant cells by linking a
XX	ubiquitin monomer coding sequence upstream of the gene encoding the
XX	desired protein.
XX	
XX	Claim 7; Page 18; 42pp; English.
XX	
XX	This sequence represents the C-terminal fragment of a ubiquitin monomer.
XX	The invention relates to a method for enhancing production of a desired
XX	protein in a plant or plant cell by inserting a nucleic acid (NA)
XX	encoding a ubiquitin monomer upstream of a NA encoding the desired
XX	protein, where the fusion construct encodes a fusion protein and
XX	expression is not controlled by the ubiquitin promoter. The invention
XX	also relates to a NA acid vector a NA vector able to transform a plant
XX	cell, that comprises NA encoding a fusion protein having a ubiquitin
XX	monomer linked to a protein of interest and further, where expression of
XX	the fusion construct is not under control of a ubiquitin promoter. The
XX	construct allows enhanced production of the desired protein in plants or
XX	plant cells

SQ Sequence 14 AA;

Query Match 100.0%; Score 69; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSAGRNR 14
|||
Db 1 MDKSESTSAGRNR 14

RESULT 2
AAR10652

ID AAR10652 standard; protein; 218 AA.

XX AAR10652;

XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-APR-1991 (first entry)

XX Capsid protein of Cucumber Mosaic Virus strain FNY.

XX CMV; resistance; capsid protein; Cucumis melo.

XX Cucumber mosaic virus.

XX EP412912-A.

XX 13-FEB-1991.

XX 09-AUG-1990; 90EP-00402282.

XX 11-AUG-1989; 89FR-00010848.

XX (BIOC-) BIOCEM SA.

XX Deboth M, Bentahar S, Noel M, Perret J;

XX WPI; 1991-046027/07.

DR N-PSDB; AAQ10461.

PT Transgenic melon plantlets prodn. from transformed shoots - by two=stage
PT culture on specific medium for new transformed plants etc., esp.
PT resistant to cucumber mosaic virus.

PS Claim 15; Page 17; 44pp; French.

CC The gene encoding this protein was isolated from a plasmid (pUC18)
CC containing DNA complementary to RNA 3 of the virulent strain FNY,
CC isolated in New York on infected melons. Transgenic melon plantlets
CC containing the nucleotide sequence introduced via an Agrobacterium
CC tumefaciens intermediate are cultured as shoots in special media. The
CC transformed melon plants are resistant to CMV. See also AAQ10462.
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
CC correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

SQ Sequence 218 AA;

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSAGRNR 14
|||
Db 1 MDKSESTSAGRNR 14

RESULT 3
AAR10653

ID AAR10653 standard; protein; 218 AA.

XX AAR10653;

XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-APR-1991 (first entry)

XX Capsid protein of Cucumber Mosaic Virus strain 117F.

XX CMV; strain 117F; resistance; capsid protein; Cucumis melo.

XX Cucumber mosaic virus.

XX EP412912-A.

XX 13-FEB-1991.

XX 09-AUG-1990; 90EP-00402282.

XX 11-AUG-1989; 89FR-00010848.

XX (BIOC-) BIOCEM SA.

XX Deboth M, Bentahar S, Noel M, Perret J;

XX WPI; 1991-046027/07.

DR N-PSDB; AAQ10462.

PT Transgenic melon plantlets prodn. from transformed shoots - by two=stage
PT culture on specific medium for new transformed plants etc., esp.
PT resistant to cucumber mosaic virus.

PS Claim 16; Page 19; 44pp; French.

CC The gene encoding this protein was isolated from the virulent French
CC strain 117F of CMV. Transgenic melon plantlets containing the coding
CC sequence (introduced via an Agrobacterium tumefaciens intermediate) are
CC cultured as shoots in special media. The transformed melon plants are
CC resistant to CMV. See also AAQ10461. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC AUG-2003 to correct OS field.)

SQ Sequence 218 AA;

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSAGRNR 14
|||
Db 1 MDKSESTSAGRNR 14

RESULT 4
AAR57968

ID AAR57968 standard; protein; 218 AA.

XX AAR57968;

XX 25-MAR-2003 (revised)
DT 20-APR-1995 (first entry)

XX Cauliflower mosaic virus capsid protein.

XX Cauliflower mosaic virus; CMV; capsid protein; coat protein;
KW polyribozyme; inactivate; inactivation; resistance; crop protection.

XX Cauliflower mosaic virus.

XX FR2701960-A1.

XX 02-SEP-1994.

XX 26-FEB-1993; 93FR-00002269.

PR 26-FEB-1993; 93FR-00002269.
XX
XX (GENE-) GENE SHEARS PTY LTD.
XX
XX Lenee P, Perez P, Gruber V, Baudot G, Ollivo C;
XX WPI; 1994-281767/35.
DR N-PSDB; AAQ67395.
XX
XX New polyribozyme contg. several catalytic regions in complementary
PT sequence - can inactivate gene for viral capsid protein, esp. for pregn.
PT of new virus resistant transgenic plants, also DNA sequence encoding it.
XX
XX Disclosure; Fig 2; 67pp; French.
XX
XX The RNA encoding the capsid protein of cauliflower mosaic virus can be
CC targeted by a nucleic acid sequence called a "polyribozyme". The
CC polyribozyme has endoribonuclease activity and is able to inactivate the
CC gene encoding the viral capsid protein. The polyribozyme comprises
CC several catalytic regions derived from ribozymes and confers complete
CC resistance to virus. See AAQ67391-94. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 5
AAR67753
ID AAR67753 standard; protein; 218 AA.
XX
AC AAR67753;
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE CMV coat protein.
XX
XX Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; coat protein; CP;
KW TOMV; CMV.
XX
XX Cucumber mosaic virus.
OS
XX
XX WO9429464-A1.
PN
XX
PD 22-DEC-1994.
XX
XX 03-JUN-1994; 94WO-EP001817.
PF
XX
XX 04-JUN-1993; 93GB-00011593.
PR
XX
XX (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
XX De Haan PT;
PI
XX
XX WPI; 1995-036490/05.
DR N-PSDB; AAQ76106.
XX
XX DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.

XX
PS Disclosure; Page 30; 50pp; English.
XX
XX A chimeric cucumber mosaic virus RNA-3 (given in AAQ76106) codes for the
CC coat protein (CP) of tomato mosaic virus (AAR67552) as well as its own CP
CC (AAR67753). The construct elicits minus-sense RNA that interacts with the
CC RNA-dependent RNA-polymerase of an invading virus, thus conferring virus-
CC resistance on a host plant, e.g. tobacco, tomato. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 6
AAR93803
ID AAR93803 standard; protein; 218 AA.
XX
XX AAR93803;
AC
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
XX Coat protein of the A35 strain of cucumber mosaic virus.
DE
XX
XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KW resistance.
KW Cucumber mosaic virus; strain A35.
XX
XX WO9621018-A1.
PN
XX
PD 11-JUL-1996.
XX
PF 07-JUN-1995; 95WO-US007234.
XX
PR 30-DEC-1994; 94US-00367789.
XX
XX (ASGR-) ASGROW SEED CO.
PA
XX
XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
PI WPI; 1996-333993/33.
XX
XX N-PSDB; AAT17259.
DR
XX
XX New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
XX Disclosure; Fig 8; 80pp; English.
PS
XX
XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
XXXXXX

Db 1 MDKSESTSAGRNR 14

RESULT 7
AAR98893
ID AAR98893 standard; protein; 218 AA.
XX
AC AAR98893;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the V27 strain of cucumber mosaic virus.
XX
KM Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance.
XX
OS Cucumber mosaic virus; strain V27.
XX
PN WO9621018-A1.
XX
PD 11-JUL-1996.
XX
PF 07-JUN-1995; 95WO-US007234.
XX
PR 30-DEC-1994; 94US-00367789.
XX
PA (ASGR-) ASGROW SEED CO.
XX
PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
DR WPI; 1996-333993/33.
DR N-PSDB; AAT34664.
XX
XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
XX
PS Disclosure; Fig 1; 80pp; English.
XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 8
AAR98894
ID AAR98894 standard; protein; 218 AA.
XX
AC AAR98894;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the V33 strain of cucumber mosaic virus.
XX
KM Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance.
XX
OS Cucumber mosaic virus; strain V33.

XX
PN WO9621018-A1.
XX
PD 11-JUL-1996.
XX
PF 07-JUN-1995; 95WO-US007234.
XX
PR 30-DEC-1994; 94US-00367789.
XX
PA (ASGR-) ASGROW SEED CO.
XX
PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
DR WPI; 1996-333993/33.
DR N-PSDB; AAT34665.
XX
XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
XX
PS Disclosure; Fig 2; 80pp; English.
XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 9
AAR98895
ID AAR98895 standard; protein; 218 AA.
XX
AC AAR98895;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the V34 strain of cucumber mosaic virus.
XX
KM Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance.
XX
OS Cucumber mosaic virus; strain V34.
XX
PN WO9621018-A1.
XX
PD 11-JUL-1996.
XX
PF 07-JUN-1995; 95WO-US007234.
XX
PR 30-DEC-1994; 94US-00367789.
XX
PA (ASGR-) ASGROW SEED CO.
XX
PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
DR WPI; 1996-333993/33.
DR N-PSDB; AAT34666.
XX
XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are

PT resistant to infection.
XX
XX Disclosure; Fig 3; 80pp; English.
PS
XX
XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 10
ABB80503
ID ABB80503 standard; protein; 218 AA.

AC ABB80503;

DT 25-JUL-2002 (first entry)

DE Agrobacterium tumefaciens protein sequence.

KW Agrobacterium tumefaciens; anti-cucumber mosaic virus; transgenic tomato.

OS Agrobacterium tumefaciens.

PN KR9075101-A.

PD 05-OCT-1999.

PF 17-MAR-1998; 98KR-00009096.

PR 17-MAR-1998; 98KR-00009096.

PA (RURA-) RURAL DEV ADMINISTRATION.

PI Sohn SH, Lee SW, Park JS, Hwang YS;

DR WPI; 2000-577926/54.

DR N-PSDB; ABL58209.

PT Anti-cucumber mosaic virus tomato.

PS Disclosure; Page 4; 6pp; Korean.

CC This sequence represents a protein sequence from Agrobacterium

CC tumefaciens used within the scope of the invention. The invention relates

XX to an anti-cucumber mosaic virus tomato

XX Sequence 218 AA;

Query Match 88.4%; Score 61; DB 3; Length 218;
Best Local Similarity 92.9%; Pred. No. 0.018;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 11
ADO61973
ID ADO61973 standard; protein; 438 AA.

XX ADO61973;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX Transcription factor G2565, SEQ ID 440.
DE
XX
XX plant; transcription factor; transgenic plant; abiotic stress tolerance;
KW osmotic stress tolerance; cold tolerance; heat tolerance;
KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
KW glyphosate resistance; flowering; fertility; seed development.
KM
XX
XX Arabidopsis thaliana.

OS WO2004031349-A2.

PN 15-APR-2004.

PD 18-SEP-2003; 2003WO-US030292.

PF 18-SEP-2002; 2002US-0411837P.

PR 17-DEC-2002; 2002US-0434166P.

PR 24-APR-2003; 2003US-0465809P.

XX (MEND-) MENDEL BIOTECHNOLOGY INC.

PI Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;

PI Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK;

XX WPI; 2004-330163/30.

DR N-PSDB; ADO61972.

XX New recombinant polynucleotide encoding transcription factor

PT polypeptides, useful for producing transgenic plants with advantageous

PT properties compared to a reference plant.

XX Disclosure; SEQ ID NO 440; 510pp; English.

XX The present invention relates to novel plant transcription factor
CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
CC sequences can be used to produce transgenic plants, which overexpress
CC (II), where the transgenic plant has an altered trait as compared to a
CC non-transgenic plant or wild-type plant. The transgenic plant comprises
CC an altered trait selected from increased tolerance to abiotic stress,
CC increased tolerance to osmotic stress, increased tolerance to cold,
CC increased germination in cold, increased tolerance to heat, increased
CC germination in heat, increased tolerance to freezing conditions,
CC increased tolerance to low nitrogen conditions, increased tolerance to
CC low phosphate conditions, increased tolerance to disease, including
CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,
CC increased tolerance to multiple fungal pathogens, increased resistance to
CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
CC increased sensitivity to ACC, altered sugar sensing, increased tolerance
CC to sugars, altered carbon/nitrogen sensing, early flowering, late
CC flowering, altered flower structure, loss of flower determinacy, reduced
CC fertility, altered shoot meristem development, altered branching pattern,
CC altered stem morphology, altered vascular tissue structure, reduced
CC apical dominance, altered trichome density, altered trichome development,
CC altered trichome structure, altered root development, altered shade
CC avoidance, altered seed development, altered seed ripening, altered seed
CC germination, slow growth, fast growth, altered cell differentiation,
CC altered cell proliferation, altered cell expansion, altered phase change,
CC altered senescence, abnormal embryo development, altered programmed cell
CC death, lethality when overexpressed, altered necrosis patterns, increased
CC plant size, increased biomass, large seedlings, dwarfed plants, dark
CC green leaves, change in leaf shape, increased leaf size and mass, light
CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
CC altered seed coloration, altered seed size, altered seed shape, large
CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil
CC content, altered seed protein content, altered seedprenyl content,
CC altered leaf prenyl lipid content, increased anthocyanin levels, and
CC decreased anthocyanin levels. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in

CC electronic format directly from WIFO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 438 AA;

Query Match 63.8%; Score 44; DB 8; Length 438;
Best Local Similarity 64.3%; Pred. No. 37;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 MDKSESTSGARNR 14
Db 420 MDQSESTSGTSNRK 433

RESULT 12
AAR37212
ID AAR37212 standard; protein; 218 AA.
XX
AC AAR37212;
XX
DT 24-OCT-2003 (revised)
DT 26-AUG-1993 (first entry)
XX
DE Cucumber mosaic virus-W coat protein.
XX
KW CUMV-W; transformants; transgenic plant; maize; Cucurbitaceae;
KW Solanaceae; melon; squash; tomato; potato; tobacco.
XX
OS Cucumber mosaic virus; W.
XX
PN ZA9104563-A.
XX
PD 25-MAR-1992.
XX
PF 16-MAR-1990; 90ZA-00002044.
XX
PR 14-JUN-1991; 91ZA-00004563.
XX
PA (AFRI) AECT LTD.
PA (UYCA-) UNITV OF CAPE TOWN.
XX
PI Thomson JA, Hackland AF, Kunert KJ, Collad DDA, Rybicki EP;
XX
DR WPI; 1992-151218/18.
DR N-PSDB; AAQ41742.
XX
PT Protecting plants against cucumber mosaic virus infection - relates to
PT e.g. isolated coat protein of virus strain and isolated DNA.
XX
PS Claim 4; Fig 2; 18pp; English.
XX
CC The 3' terminal 140-320 bases of the segmental genome RNA sequences of
CC Bromovirus, Alfalfa mosaic virus and Cucumovirus (including CUMV) show a
CC high degree of homology and this information was used to design a primer
CC (see AAQ41743) complementary to part of the 3' terminal non coding region
CC of the RNA3 (encodes the coat protein) of CUMV-Q which was used to prime
CC synthesis of a cDNA sequence using RNA3 of CUMV-W as a template. The ds
CC cDNA corresp. to RNA3 of CUMV-W was introduced into plasmid pUC19 and
CC used to transform E. coli. Transformants contg. an insert of 800 bp were
CC selected and sequenced. The CUMV-W coat protein gene sequence may be used
CC to transform plants to produce transgenic plants with resistance to CUMV
CC infection. Protected plants are pref. maize or from Cucurbitaceae or
CC Solanaceae species, e.g. cucumber, melon, squash, tomato, potato or
CC tobacco. (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 218 AA;

Query Match 60.9%; Score 42; DB 2; Length 218;
Best Local Similarity 64.3%; Pred. No. 39;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 MDKSESTSGARNR 14
|||||||:| |

Db 1 MDKSESPNASRTSR 14

RESULT 13
AAG05253
ID AAG05253 standard; protein; 289 AA.
XX
AC AAG05253;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1590.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX

PF 25-FEB-2000; 2000EP-00301439.
XX
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
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PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
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PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
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PR 22-JUL-1999; 99US-0145089P.
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PR 23-JUL-1999; 99US-0145218P.
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PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
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PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.

PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
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PR 26-AUG-1999; 99US-0150884P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
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PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 58.0%; Score 40; DB 3; Length 289;
Best Local Similarity 72.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 DKSESTSAGRN 12
Db 17 DSSSSSSSAGRN 27

RESULT 14
AAG00746
ID AAG00746 standard; protein; 64 AA.
XX

AC AAG00746;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 4827.
XX
KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI, 2000-500381/45.
DR N-PSDB; AAC00752.
XX
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX
PS Claim 13; SEQ ID NO 4827; 71pp + Sequence Listing; English.
XX
CC The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX
SQ Sequence 64 AA;
Query Match 56.5%; Score 39; DB 3; Length 64;
Best Local Similarity 58.3%; Pred. No. 36;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 3 KSESTSAGRNR 14
:||||:|:|:|
Db 53 QSESTNGKNKR 64
RESULT 15
ABOS7865
ID ABO57865 standard; protein; 68 AA.
XX
AC ABO57865;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon protein #4099.
XX
KM Human; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
PN US2003194704-A1.

XX
PD 16-OCT-2003.
XX
PF 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
DR WPI; 2004-119264/12.
XX
PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
XX
PS Claim 45; SEQ ID NO 31499; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 688 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20030194704
XX
SQ Sequence 68 AA;
Query Match 56.5%; Score 39; DB 8; Length 68;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 3 KSESTSAGRNR 14
:||||:|:|:|
Db 31 QSESTNGKNKR 42
Search completed: December 5, 2004, 08:05:23
Job time : 74 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2004, 07:34:22 ; Search time 23 Seconds
(without alignments)
58.567 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSAGRNR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	69	100.0	218	1	JQ1253	coat protein - cuc
2	69	100.0	218	1	JQ1254	coat protein - cuc
3	69	100.0	218	1	JS0090	coat protein - cuc
4	69	100.0	218	1	VCVXY1	coat protein - cuc
5	69	100.0	218	2	JC6075	coat protein - cuc
6	69	100.0	218	2	S42098	coat protein - cuc
7	69	100.0	218	2	S58039	capsid protein - cuc
8	69	100.0	218	2	JC6074	coat protein - cuc
9	69	100.0	218	2	JC6073	coat protein - cuc
10	69	100.0	218	2	S09663	coat protein - cuc
11	64	92.8	218	1	JA0136	coat protein - cuc
12	64	92.8	218	2	D71392	coat protein - cuc
13	41	59.4	1711	2	T21432	hypothetical prote
14	39	56.5	1473	2	T31422	C-terminal domain-
15	38	55.1	38	2	B83765	hypothetical prote
16	38	55.1	44	2	B44365	sperm receptor lig
17	38	55.1	178	2	E95994	hypothetical prote
18	38	55.1	210	2	A56844	POM-ZP3 protein -
19	38	55.1	562	2	T29858	hypothetical prote
20	38	55.1	1511	2	S60932	probable membrane
21	38	55.1	1672	2	T46237	hypothetical prote
22	37	53.6	64	1	WMWQTD	p7a protein - toba
23	37	53.6	124	2	T04505	hypothetical prote
24	37	53.6	1876	2	E97944	zinc metalloprotei
25	36	52.2	169	2	AF2743	conserved hypotet
26	36	52.2	169	2	E97524	hypothetical prote
27	36	52.2	232	2	H95144	ribonuclease III (
28	36	52.2	232	2	F98012	ribonuclease III (
29	36	52.2	349	2	T07396	probable outward r

30	36	52.2	432	2	D86937	probable membrane
31	36	52.2	497	2	C82025	probable periplasm
32	36	52.2	671	2	C96546	probable GTP-bindi
33	36	52.2	758	2	E81217	organic solvent to
34	36	52.2	779	2	T34390	hypothetical prote
35	36	52.2	802	2	B81794	probable solvent t
36	36	52.2	1532	2	A61262	collagen alpha 1(X
37	36	52.2	1908	2	A86311	protein F13.14 [i
38	35.5	51.4	1194	1	DJBE28	DNA-directed DNA p
39	35	50.7	111	2	A87525	BF hand domain pro
40	35	50.7	177	2	F72715	hypothetical prote
41	35	50.7	218	1	B46111	coat protein - cuc
42	35	50.7	218	1	VCVXUV	coat protein - cuc
43	35	50.7	218	1	VCVXWL	coat protein - cuc
44	35	50.7	248	2	T04758	hypothetical prote
45	35	50.7	330	2	F72209	hypothetical prote

ALIGNMENTS

RESULT 1
JQ1253
coat protein - cucumber mosaic virus (strain FC)
C/Species: cucumber mosaic virus, CMV
C/Date: 31-Mar-1992 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C/Accession: JQ1253
R/Shintaku, M.
J. Gen. Virol. 72, 2587-2589, 1991
A/Title: Coat protein gene sequences of two cucumber mosaic virus strains reveal a single
A/Reference number: JQ1253; MUID:92013983; PMID:1919534
A/Accession: JQ1253
A/Molecule type: genomic RNA
A/Residues: 1-218 <SHI>
A/Cross-references: UNIPROT:Q00259; GB:D10544; NID:g222024; PIDN:BA01403.1; PID:g222025
A/Note: comparison of the amino acid sequence of this protein to that of strain P6 shows
R/Tsunasawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A/Title: Micro-identification of amino-terminal acetyl amino acids in proteins.
A/Reference number: A61297; MUID:83056735; PMID:6754709
A/Contents: annotation; acetylation
C/Comment: This cucumber mosaic virus strain induces a yellow chlorosis.
C/Superfamily: cucumber mosaic virus coat protein
C/Keywords: acetylated amino end; coat protein
F/1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 2
JQ1254
coat protein - cucumber mosaic virus (strain P6)
C/Species: cucumber mosaic virus, CMV
C/Date: 31-Mar-1992 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C/Accession: JQ1254
R/Shintaku, M.
J. Gen. Virol. 72, 2587-2589, 1991
A/Title: Coat protein gene sequences of two cucumber mosaic virus strains reveal a single
A/Reference number: JQ1253; MUID:92013983; PMID:1919534
A/Accession: JQ1254
A/Molecule type: genomic RNA
A/Residues: 1-218 <SHI>
A/Cross-references: UNIPROT:Q00261; GB:D10545; NID:g222026; PIDN:BA01404.1; PID:g222027
A/Note: comparison of the amino acid sequence of this protein to that of strain FC shows
R/Tsunasawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A/Title: Micro-identification of amino-terminal acetyl amino acids in proteins.

A;Reference number: A61297; MUID:83056735; PMID:6754709
A;Contents: annotation; acetylation
C;Comment: This cucumber mosaic virus strain induces a yellow chlorosis.
C;Superfamily: cucumber mosaic virus coat protein
C;Keywords: acetylated amino end; coat protein
F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 3

JS0090 coat protein - cucumber mosaic virus (strain O)

C;Species: cucumber mosaic virus, CMV
C;Date: 31-Mar-1992 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C;Accession: JS0090; PS0314

R;Hayakawa, T.; Mizukami, M.; Nakajima, M.; Suzuki, M.
J. Gen. Virol. 70, 499-504, 1989

A;Title: Complete nucleotide sequence of RNA 3 from cucumber mosaic virus (CMV) strain C
A;Reference number: JS0089; MUID:89279231; PMID:2732698
A;Accession: JS0090

A;Molecule type: mRNA
A;Residues: 1-218 <HA>

A;Cross-references: UNIPROT:P16489; GB:D00385; NID:g222030; PIDN:BA00297.1; PID:g222032
A;Accession: PS0314

A;Molecule type: protein
A;Residues: 216-218 <HA2>

R;Tsunasawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982

A;Title: Micro-identification of amino-terminal acetylamino acids in proteins.
A;Reference number: A61297; MUID:83056735; PMID:6754709

A;Contents: annotation; acetylation
C;Genetics:

A;Map position: segment 3
C;Superfamily: cucumber mosaic virus coat protein

C;Keywords: acetylated amino end; coat protein
F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 4

VCVXY1

coat protein - cucumber mosaic virus (strain Y)

C;Species: cucumber mosaic virus, CMV
A;Note: host Nicotiana tabacum cv. Xanthi nc (tobacco)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004

C;Accession: JA0097
R;Nitta, N.; Masuta, C.; Kuwata, S.; Takanami, Y.

Ann. Phytopathol. Soc. Jpn. 54, 516-522, 1989

A;Title: Comparative studies on the nucleotide sequence of cucumber mosaic virus RNA3 be
A;Reference number: JA0096

A;Accession: JA0097
A;Molecule type: mRNA

A;Residues: 1-218 <NIT>
A;Cross-references: UNIPROT:P18027
R;Tsunasawa, S.; Narita, K.

J. Biochem. 92, 607-613, 1982

A;Title: Micro-identification of amino-terminal acetylamino acids in proteins.
A;Reference number: A61297; MUID:83056735; PMID:6754709

A;Contents: annotation; acetylation

C;Comment: The genome consists of three single-stranded, positive RNAs, designated RNA1,
C;Genetics:
A;Map position: segment RNA3
C;Superfamily: cucumber mosaic virus coat protein
C;Keywords: acetylated amino end; coat protein
F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 5

JC6075 coat protein - cucumber mosaic virus (strain CS)

C;Species: cucumber mosaic virus, CMV
C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC6075

R;Huaping, L.; Hu, J.S.; Barry, K.; Hweichung, F.
Chinese J. Virol. 12, 235-242, 1996

A;Title: Coat protein gene sequence analysis of three cucumber mosaic virus strains infec
A;Reference number: JC6073
A;Accession: JC6075

A;Molecule type: mRNA
A;Residues: 1-218 <HUA>

A;Cross-references: UNIPROT:Q8JFX2; UNIPROT:Q9DJX2; UNIPROT:Q91PK5; UNIPROT:Q9DJX3; UNIP
ROT:Q8JFX0; UNIPROT:Q9DJW5; UNIPROT:Q91PP6; UNIPROT:Q8JFX4; UNIPROT:Q9DJ
6132; UNIPROT:Q9YJS2; UNIPROT:Q8JFW8; UNIPROT:Q9ENS6; UNIPROT:Q93259; UNIPROT:Q9DWW2; UN

A;Experimental source: strain CS
A;Note: the authors translated the codon CCG for residue 83 as Gly

C;Genetics:
A;Gene: cp

C;Superfamily: cucumber mosaic virus coat protein
C;Keywords: coat protein

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 6

S42098

coat protein - cucumber mosaic virus

C;Species: cucumber mosaic virus, CMV
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S42098

R;Hyon, S.; Park, Y.I.
submitted to the EMBL Data Library, February 1994

A;Description: Nucleotide sequence of cDNA from RNA4 of cucumber mosaic virus-As the Kore
A;Reference number: S42098
A;Accession: S42098

A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-218 <HYO>
A;Cross-references: UNIPROT:Q66154; EMBL:X77855; NID:g457166; PIDN:CAA54846.1; PID:g45716

C;Superfamily: cucumber mosaic virus coat protein

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 7

S58039

capsid protein - cucumber mosaic virus

C;Species: cucumber mosaic virus, CMV

C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C;Accession: S58039

R;Haq, Q.M.R.

submitted to the EMBL Data Library, July 1995

A;Reference number: S58039

A;Accession: S58039

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-218 <HAQ>

A;Cross-references: UNIPROT:Q66157; EMBL:X89652; NID:g902619; PIDN:CAA61802.1; PID:g9026

C;Superfamily: cucumber mosaic virus coat protein

Query Match 100.0%; Score 69; DB 2; Length 218;

Best Local Similarity 100.0%; Pred. No. 3.6e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNRR 14

Db 1 MDKSESTSGRNRR 14

RESULT 8

JC6074

coat protein - cucumber mosaic virus (strain MM)

C;Species: cucumber mosaic virus, CMV

C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004

C;Accession: JC6074

R;Huaping, L.; Hu, J.S.; Barry, K.; Hweichung, F.

Chinese J. Virol. 12, 235-242, 1996

A;Title: Coat protein gene sequence analysis of three cucumber mosaic virus strains infe

A;Reference number: JC6073

A;Accession: JC6074

A;Molecule type: mRNA

A;Residues: 1-218 <HUA>

A;Cross-references: UNIPROT:Q83257; UNIPROT:O55251; UNIPROT:Q9WAB3; UNIPROT:Q9YJR9; UNIF

A;Experimental source: strain MM

A;Note: the authors translated the codon CGT for residue 30 as Ala

C;Genetics:

A;Gene: cp

C;Superfamily: cucumber mosaic virus coat protein

C;Keywords: coat protein

Query Match 100.0%; Score 69; DB 2; Length 218;

Best Local Similarity 100.0%; Pred. No. 3.6e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNRR 14

Db 1 MDKSESTSGRNRR 14

RESULT 9

JC6073

coat protein - cucumber mosaic virus (strain BS)

C;Species: cucumber mosaic virus, CMV

C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004

C;Accession: JC6073

R;Huaping, L.; Hu, J.S.; Barry, K.; Hweichung, F.

Chinese J. Virol. 12, 235-242, 1996

A;Title: Coat protein gene sequence analysis of three cucumber mosaic virus strains infe

A;Reference number: JC6073

A;Accession: JC6073

A;Molecule type: mRNA

A;Residues: 1-218 <HUA>

A;Cross-references: UNIPROT:Q9DUW8; UNIPROT:Q9YJR7; UNIPROT:Q8JPK1; UNIPROT:Q9E2V6; UNIF

PROT:Q91PP6; UNIPROT:Q9JFY4; UNIPROT:Q66157; UNIPROT:O66130; UNIPROT:O8JPK4; UNIPROT:Q9D

6132; UNIPROT:Q9YJS2; UNIPROT:Q8JPK8; UNIPROT:Q9ENS6; UNIPROT:Q83259; UNIPROT:Q9DWM2; UN

A;Experimental source: strain BS

A;Note: the authors translated the codon CCA for residue 56 as Thr and CCC for residue 5;

C;Genetics:

A;Gene: cp

C;Superfamily: cucumber mosaic virus coat protein

C;Keywords: coat protein

Query Match 100.0%; Score 69; DB 2; Length 218;

Best Local Similarity 100.0%; Pred. No. 3.6e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNRR 14

Db 1 MDKSESTSGRNRR 14

RESULT 10

S09663

coat protein - cucumber mosaic virus (strain I17F)

C;Species: cucumber mosaic virus, CMV

A;Variety: strain I17F

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S09663; S06932

R;Noel, M.J.T.; Tahar, S.B.

Nucleic Acids Res. 18, 1332, 1990

A;Title: Corrigendum. Nucleotide sequence of the coat protein gene and flanking regions c

A;Reference number: S09663; MUID:90206832; PMID:2320436

A;Accession: S09663

A;Molecule type: mRNA

A;Residues: 1-218 <NOE>

A;Cross-references: UNIPROT:P14767

A;Experimental source: strain I17F

A;Note: this is a revision to the sequence from reference S06932

R;Noel, M.J.T.; Tahar, S.B.

Nucleic Acids Res. 17, 10492, 1989

A;Title: Nucleotide sequence of the coat protein gene and flanking regions of Cucumber Mc

A;Reference number: S06932; MUID:90098885; PMID:2602158

A;Accession: S06932

A;Molecule type: mRNA

A;Residues: 1-6, 'W', 8-44, 'W', 46-51, 'W', 53-56, 'W', 58-68, 'W', 70, 'W', 72-73, 'W', 75-96, 'W', 98-

A;Cross-references: EMBL:X16386

A;Experimental source: strain I17F

A;Note: this sequence has been revised in reference S09663

C;Superfamily: cucumber mosaic virus coat protein

Query Match 100.0%; Score 69; DB 2; Length 218;

Best Local Similarity 100.0%; Pred. No. 3.6e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNRR 14

Db 1 MDKSESTSGRNRR 14

RESULT 11

JA0136

coat protein - cucumber mosaic virus (strain C)

C;Species: cucumber mosaic virus, CMV

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: JA0136

R;Quemada, H.; Kearney, C.; Gonsalves, D.; Slightom, J.L.

J. Gen. Virol. 70, 1065-1073, 1989

A;Title: Nucleotide sequences of the coat protein genes and flanking regions of cucumber

A;Reference number: JU0087; MUID:89279284; PMID:2732712

A;Accession: JA0136

A;Molecule type: genomic RNA

A;Residues: 1-218 <QUE>

A;Cross-references: UNIPROT:P21368; GB:D00462; NID:g222041; PIDN:BAA00357.1; PID:g222042

R;Tsunasawa, S.; Narita, K.

J. Biochem. 92, 607-613, 1982

A;Title: Micro-identification of amino-terminal acetyl amino acids in proteins.

A;Reference number: A61297; MUID:83056735; PMID:6754709

A;Contents: annotation; acetylation

C;Genetics:

A;Map position: segment RNA3
C;Superfamily: cucumber mosaic virus coat protein
C;Keywords: acetylated amino end; coat protein; glycoprotein
F;1/Modified site: acetylated amino end (Met) #status experimental
F;43/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.8%; Score 64; DB 1; Length 218;
Best Local Similarity 92.9%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 12
D71392
coat protein - cucumber mosaic virus (strain Ixora)
N;Alternate names: capsid protein
C;Species: cucumber mosaic virus, CMV
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Accession: D71392
R;McGarvey, P.; Touseignant, M.; Gelecka, L.; Cellini, F.; Kaper, J.M.
J. Gen. Virol. 76, 2257-2270, 1995
A;Title: The complete sequence of a cucumber mosaic virus from Ixora that is deficient i
A;Reference number: A71392; MUID:9605047; PMID:7561763
A;Accession: D71392
A;Molecule type: mRNA
A;Residues: 1-218 <MCG>
A;Cross-references: UNIPROT:Q66120; GB:U20219; NID:g1161916; PIDN:AAC54619.1; PID:g11619
A;Experimental source: strain Ixora
C;Comment: The CMV genome consists of three species of single-stranded, capped, positive
C;Comment: The Ixora strain in unusual in that it does not replicate several well charac
ptoms found when replicated by other CMV strains.
C;Genetics:
A;Map position: segment RNA 3
C;Superfamily: cucumber mosaic virus coat protein
C;Keywords: acetylated amino end; coat protein
F;1/Modified site: acetylated amino end (Met) #status predicted

Query Match 92.8%; Score 64; DB 2; Length 218;
Best Local Similarity 92.9%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 13
T21432
hypothetical protein F26H1.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21432
R;Barlow, K.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19421
A;Accession: T21432
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1711 <WIL>
A;Cross-references: UNIPROT:O45409; EMBL:Z81515; PIDN:CAB04197.1; GSPDB:GN00020; CESP:FZ
A;Experimental source: clone F26H1
C;Genetics:
A;Gene: CESP:F26H1.2
A;Map position: 2
A;introns: 56/3; 154/2; 373/2; 417/3; 505/2; 596/1; 703/2; 847/3; 922/3; 1034/2; 1078/2;

Query Match 59.4%; Score 41; DB 2; Length 1711;
Best Local Similarity 69.2%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 DKSESTSAGRNR 14
Db 82 DPSESTSSSRPR 94

RESULT 14
T31422
C-terminal domain-binding protein RA9 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31422
R;Yuryev, A.; Paturajan, M.; Litington, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Corde
Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996
A;Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts with
A;Reference number: Z21024; MUID:96293459; PMID:8692929
A;Accession: T31422
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1473 <YUR>
A;Cross-references: UNIPROT:Q63625; EMBL:U49057; NID:g1438533; PID:g1438534; PIDN:AAC526;
A;Experimental source: hippocampus

Query Match 56.5%; Score 39; DB 2; Length 1473;
Best Local Similarity 57.1%; Pred. No. 85;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 MDKSESTSAGRNR 14
Db 944 MDKESMTSRERR 957

RESULT 15
B83765
hypothetical protein BH0922 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: B83765
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83765
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-38 <STO>
A;Cross-references: UNIPROT:Q9KED1; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA046;
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0922

Query Match 55.1%; Score 38; DB 2; Length 38;
Best Local Similarity 53.8%; Pred. No. 3.5;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 MDKSESTSAGRNR 13
Db 1 MDKQRMAGRNRR 13

Search completed: December 5, 2004, 08:05:50.
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2004, 07:59:17 ; Search time 91 Seconds
(without alignments)
88.519 Million cell updates/sec

Title: US-09-857-841-4

Perfect score: 69
Sequence: 1 MDKSESTSAGRNR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	217	2 Q6T7D4	Q6T7D4 cucumber mo
2	69	100.0	217	2 Q66133	Q66133 cucumber mo
3	69	100.0	217	2 Q8QTA0	Q8QTA0 banana mosa
4	69	100.0	217	2 AAR89478	AAR89478 cucumber
5	69	100.0	218	1 COAT_CMVAS	Q66154 cucumber mo
6	69	100.0	218	1 COAT_CMVBA	Q66135 cucumber mo
7	69	100.0	218	1 COAT_CMVC7	Q40983 cucumber mo
8	69	100.0	218	1 COAT_CMVCS	Q66143 cucumber mo
9	69	100.0	218	1 COAT_CMVFC	Q00259 cucumber mo
10	69	100.0	218	1 COAT_CMVFT	Q66140 cucumber mo
11	69	100.0	218	1 COAT_CMVII	P14767 cucumber mo
12	69	100.0	218	1 COAT_CMVII	Q83271 cucumber mo
13	69	100.0	218	1 COAT_CMVKO	Q83269 cucumber mo
14	69	100.0	218	1 COAT_CMVM	Q00260 cucumber mo
15	69	100.0	218	1 COAT_CMVN	Q66138 cucumber mo
16	69	100.0	218	1 COAT_CMVNT	Q40980 cucumber mo
17	69	100.0	218	1 COAT_CMVO	P16489 cucumber mo
18	69	100.0	218	1 COAT_CMVP6	Q00261 cucumber mo
19	69	100.0	218	1 COAT_CMVY	P18027 cucumber mo
20	69	100.0	218	2 Q89125	Q89125 cucumber mo
21	69	100.0	218	2 Q90712	Q90712 cucumber mo
22	69	100.0	218	2 Q6Q4B0	Q6Q4B0 cucumber mo
23	69	100.0	218	2 Q6QHD0	Q6QHD0 cucumber mo
24	69	100.0	218	2 Q6S5T9	Q6S5T9 cucumber mo
25	69	100.0	218	2 Q6T7E2	Q6T7E2 cucumber mo
26	69	100.0	218	2 Q6U1J9	Q6U1J9 cucumber mo
27	69	100.0	218	2 Q6U1R4	Q6U1R4 cucumber mo
28	69	100.0	218	2 Q6U1R5	Q6U1R5 cucumber mo
29	69	100.0	218	2 Q6U6T0	Q6U6T0 cucumber mo
30	69	100.0	218	2 Q6U7I8	Q6U7I8 cucumber mo
31	69	100.0	218	2 Q6UB07	Q6UB07 cucumber mo

32	69	100.0	218	2 Q76U37	Q76U37 cucumber mo
33	69	100.0	218	2 Q7TDD9	Q7TDD9 cucumber mo
34	69	100.0	218	2 Q7TDV0	Q7TDV0 cucumber mo
35	69	100.0	218	2 Q7THU8	Q7THU8 cucumber mo
36	69	100.0	218	2 Q66131	Q66131 cucumber mo
37	69	100.0	218	2 Q66132	Q66132 cucumber mo
38	69	100.0	218	2 Q66155	Q66155 cucumber mo
39	69	100.0	218	2 Q66157	Q66157 cucumber mo
40	69	100.0	218	2 Q83257	Q83257 cucumber mo
41	69	100.0	218	2 Q83258	Q83258 cucumber mo
42	69	100.0	218	2 Q83259	Q83259 cucumber mo
43	69	100.0	218	2 Q83260	Q83260 cucumber mo
44	69	100.0	218	2 Q8JJK5	Q8JJK5 cucumber mo
45	69	100.0	218	2 Q8JNX8	Q8JNX8 cucumber mo

ALIGNMENTS

RESULT 1

Q6T7D4	PRELIMINARY;	PRT;	217 AA.
ID Q6T7D4			
AC Q6T7D4			
DT 05-JUL-2004 (TREMBLrel. 27, Created)			
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE Coat protein.			
OS Cucumber mosaic virus (cucumber mosaic cucumovirus).			
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;			
OC Cucumovirus.			
OX NCBI_TaxID=12305;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Yan L., Xu Z., Goldbach R., Chen K., Prins M.,			
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AY429437; AAR89478.1; .			
DR GO; GO:0019028; C:Viral capsid; IEA.			
DR GO; GO:0005198; F:Structural molecule activity; IEA.			
DR InterPro; IPR000247; Cucumovirus_coat.			
DR InterPro; IPR008975; Viral_cap_coat.			
DR Pfam; PF00760; Cucumo_coat; 1.			
DR PRINTS; PR00222; CUCUMOCOAT.			
DR ProDom; PD001284; Cucumovirus_coat; 1.			
KW Coat protein.			
SQ SEQUENCE 217 AA; 24015 MW; 32D0035BAF20E891 CRC64;			

Query Match 100.0%; Score 69; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 2

Q66133	PRELIMINARY;	PRT;	217 AA.
ID Q66133			
AC Q66133			
DT 01-NOV-1996 (TREMBLrel. 01, Created)			
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Coat protein.			
OS Cucumber mosaic virus (cucumber mosaic cucumovirus).			
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;			
OC Cucumovirus.			
OX NCBI_TaxID=12305;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Reichel H., Marino L., Kummert J., Belalcazar S., Narvaez J.;			
RT "Caracterización del gen de la proteína de la capsida de dos			
RT aislamientos del virus del mosaico del pepino (CMV), obtenidos de			
RT platano y banana (Musa spp.).";			

RL Revista Corpolca 1:1-5(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Marino-Ramirez L.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U32859; AAB50176.1; -.
DR PIR; JC6073; JC6073.
DR PIR; JC6075; JC6075.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:005198; F:structural molecule activity; IEA.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 217 AA; 24015 MW; 7251B7E67192DCAB CRC64;

Query Match 100.0%; Score 69; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 3
ID Q8QTA0 PRELIMINARY; PRT; 217 AA.
AC Q8QTA0;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Coat protein.
OS Banana mosaic virus.
OC Viruses; unclassified viruses.
OX NCBI_TaxID=179820;
RN [1]
RP SEQUENCE FROM N.A.
RA Daolin D., Jie S., Peng Z., Zhixin L., Xiaodong D., Xueqing Z.;
RT "Cloning and Reconstruction of a Expression Vector for the Banana
RT Mosaic Virus Coat Protein Gene";
RL Guangxi Zhi wu 0:0-0(2002).
DR EMBL; AF444252; AAL48223.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:005198; F:structural molecule activity; IEA.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 217 AA; 23739 MW; 3873A80567D3B3AE CRC64;

Query Match 100.0%; Score 69; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 4
ID AAR89478 PRELIMINARY; PRT; 217 AA.
AC AAR89478;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE Coat protein.
OS Cucumber mosaic virus (cucumber mosaic cucumovirus).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=12305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS;
RA Yan L., Xu Z., Goldbach R., Chen K., Prins M.;
RT "Complete nucleotide sequence of cucumber mosaic virus (CS isolate)
RT RNA3";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY429437; AAR89478.1; -.
KW Coat protein.
SQ SEQUENCE 217 AA; 24015 MW; 32D0035B4F20E891 CRC64;

Query Match 100.0%; Score 69; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 5
ID COAT_CMVAS STANDARD; PRT; 218 AA.
AC Q66154;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumber mosaic virus (strain As) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117118;
RN [1]
RP SEQUENCE FROM N.A.
RA Hyon S., Park Y.I.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.
CC -----
CC This swiss-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X77855; CAA54846.1; -.
DR PIR; S42098; S42098.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24044 MW; E6BEC2E3D4CD73EF CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 6
ID COAT_CMVBA STANDARD; PRT; 218 AA.
AC Q66135;

DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain Banana) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117120;
RN [1]
RP SEQUENCE FROM N.A.
RA Gafny R., Wexler A., Mawassi M., Israeli Y., Bar-Joseph M.;
RT "Natural infection of banana by a satellite-containing strain of
RT cucumbe mosaic virus.";
RL Phycoparasitica 24:49-56(1996).
CC -|- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.

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DR EMBL; U43888; AAA87044.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KM Coat protein.
SQ SEQUENCE 218 AA; 24174 MW; 9EB4FCB212A21223 CRC64;
QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 7
COAT_CMV7 STANDARD; PRT; 218 AA.
AC 040983;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain C7-2) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117117;
RN [1]
RP SEQUENCE FROM N.A.
RA Chaumplik P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,
RA Suzuki K., Mise K., Inouye N., Okuno T., Furusawa I.;
RT "Six new subgroup I members of Japanese cucumbe mosaic virus as
RT determined by nucleotide sequence analysis on RNA3's cDNAs.";
RL Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).
CC -|- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.

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DR EMBL; D42079; BAA07675.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KM Coat protein.
SQ SEQUENCE 218 AA; 24033 MW; 16D96022D1A26FD8 CRC64;
QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 8
COAT_CMVCS STANDARD; PRT; 218 AA.
AC 066143;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain CS) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117109;
RN [1]
RP SEQUENCE FROM N.A.
RA Chaumplik P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,
RA Suzuki K., Mise K., Inouye N., Okuno T., Furusawa I.;
RT "Six new subgroup I members of Japanese cucumbe mosaic virus as
RT determined by nucleotide sequence analysis on RNA3's cDNAs.";
RL Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).
CC -|- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.

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DR EMBL; D28489; BAA05851.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KM Coat protein.
SQ SEQUENCE 218 AA; 24157 MW; 76F6BDCD9628F683 CRC64;
QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 9
COAT_CMVFC STANDARD; PRT; 218 AA.
AC 000259;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Coat protein (Capsid protein) (CP).
OS Cucumber mosaic virus (strain FC) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=31717;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013983; PubMed=1919534;
RA Shintaku M.;
RT "Coat protein gene sequences of two cucumber mosaic virus strains
RT reveal a single amino acid change correlating with chlorosis
RT induction.";
RL J. Gen. Virol. 72:2587-2589(1991).

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DR EMBL; D10544; BAA01403.1; -.
DR PIR; JQ1253; JQ1253.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24130 MW; C4B7CFB12F2A7CAB CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSAGRNR 14
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Db 1 MDKSESTSAGRNR 14

RESULT 10
COAT_CMVFT STANDARD; PRT; 218 AA.
AC Q66140;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumber mosaic virus (strain FT) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117112;
RN [1]
RP SEQUENCE FROM N.A.
RA Chaumplik P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,
RA Suzuki K., Mise K., Inouye N., Okuno T., Furusawa I.;
RT "Six new subgroup I members of Japanese cucumber mosaic virus as
RT determined by nucleotide sequence analysis on RNA3's cDNAs.";
RL Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.

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DR EMBL; D28487; BAA05847.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.

DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24160 MW; 5D3B98298E8A3997 CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSAGRNR 14
|||
Db 1 MDKSESTSAGRNR 14

RESULT 11
COAT_CMV11 STANDARD; PRT; 218 AA.
ID COAT_CMV11
AC P14767;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumber mosaic virus (strain I17F) (CMV), and
OS Cucumber mosaic virus (strain FNY) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=12308, 12307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=I17F;
RX MEDLINE=90098885; PubMed=2602158;
RA Noel M.J.T., Ben Tahar S.;
RT "Nucleotide sequence of the coat protein gene and flanking regions of
RT cucumber mosaic virus (CMV) strain I17F.";
RL Nucleic Acids Res. 17:10492-10492(1989).
RN [2]
RP ERRATUM.
RX MEDLINE=90206832; PubMed=2320436;
RA Noel M.J.T., Ben Tahar S.;
RL Nucleic Acids Res. 18:1332-1332(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FNY;
RX MEDLINE=91037954; PubMed=2230731;
RA Owen J., Shintaku M., Aeschleman P., Tahar S., Palukaitis P.;
RT "Nucleotide sequence and evolutionary relationships of cucumber mosaic
RT virus (CMV) strains: CMV RNA 3.";
RL J. Gen. Virol. 71:2243-2249(1990).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.

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DR EMBL; X16386; CAA34422.1; -.
DR EMBL; D10538; BAA01397.1; -.
DR PIR; S09663; S09663.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24140 MW; C4B4FCB21F197F98 CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;

Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGARNRR 14
|||||

Db 1 MDKSESTSGARNRR 14

RESULT 12

COAT_CMVII STANDARD; PRT; 218 AA.

ID COAT_CMVII
AC Q83271;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain Iizuka) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117113;
RN [1]
RP SEQUENCE FROM N.A.
RA Karasawa A., Ito A., Okada I., Hase S., Ehara Y.;
RT "A possible role of RNA 2 of cucumber mosaic cucumovirus as a
RT determinant of infection phenotype on cowpea."
RL Ann. Phytopathol. Soc. Jpn. 63:289-297(1997).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.

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CC -----
CC EMBL; D16405; BAA03889.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24144 MW; 087CFBFCDE90B6EB CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGARNRR 14
|||||

Db 1 MDKSESTSGARNRR 14

RESULT 13

COAT_CMVKO STANDARD; PRT; 218 AA.

ID COAT_CMVKO
AC Q83269;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain Kor) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim S.J., Cho H.S., Yu J.S., Kwon C.S., Kwon S.Y., Park E.K.,
RA Paek K.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein

CC family.
CC -----
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CC -----
CC EMBL; L36251; AAA46418.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24138 MW; 04A21106D3D43344 CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGARNRR 14
|||||

Db 1 MDKSESTSGARNRR 14

RESULT 14

COAT_CMVN STANDARD; PRT; 218 AA.

ID COAT_CMVN
AC Q00260;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain M) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=31718;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91037954; PubMed=2230731;
RA Owen J., Shintaku M., Aeschleman P., Tahar S., Palukaitis P.;
RT "Nucleotide sequence and evolutionary relationships of cucumber mosaic
RT virus (CMV) strains: CMV RNA 3."
RL J. Gen. Virol. 71:2243-2249(1990).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.

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CC -----
CC EMBL; D10539; BAA01399.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24243 MW; 75B0BFEB247C93D7 CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGARNRR 14
|||||

Db 1 MDKSESTSAGRNR 14

RESULT 15

COAT_CMVN STANDARD; PRT; 218 AA.

AC 066138;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbers mosaic virus (strain N) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117123;

RP SEQUENCE FROM N.A.
RA Chaumplik P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,
RA Suzuki K., Mise K., Inouye N., Okuno T., Furusawa I.,
RT "Six new subgroup I members of Japanese cucumber mosaic virus as
RT determined by nucleotide sequence analysis on RNA3's cDNAs.";
RL Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.

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CC -----

DR EMBL; D28486; BAA05845.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KM Coat protein.
SQ SEQUENCE 218 AA; 24078 MW; 0BA67C84D8F41B22 CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

Search completed: December 5, 2004, 08:07:27
Job time : 92 secs

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OM protein - protein search, using sw model

Run on: December 5, 2004, 08:00:12 ; Search time 23 Seconds
(without alignments)
40.367 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSAGRNR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	217	6 5422259-2	Patent No. 5422259
2	69	100.0	218	1 US-08-398-209-2	Sequence 2, Appli
3	69	100.0	218	1 US-08-398-209-4	Sequence 4, Appli
4	69	100.0	218	2 US-08-553-619B-3	Sequence 3, Appli
5	69	100.0	218	3 US-08-875-233-2	Sequence 2, Appli
6	69	100.0	218	3 US-08-875-233-4	Sequence 4, Appli
7	69	100.0	218	3 US-08-875-233-6	Sequence 6, Appli
8	69	100.0	218	3 US-08-875-233-15	Sequence 15, Appli
9	69	100.0	218	3 US-09-127-742-2	Sequence 2, Appli
10	69	100.0	218	3 US-09-127-742-4	Sequence 4, Appli
11	69	100.0	218	6 5422259-4	Patent No. 5422259
12	64	92.8	218	3 US-08-875-233-10	Sequence 10, Appli
13	39	56.5	64	4 US-09-513-999C-4827	Sequence 4827, Ap
14	39	56.5	66	3 US-08-961-564A-5	Sequence 5, Appli
15	38	55.1	172	3 US-09-382-080-3	Sequence 3, Appli
16	38	55.1	172	3 US-08-859-937-3	Sequence 3, Appli
17	37	53.6	303	4 US-09-328-352-8049	Sequence 8049, Ap
18	37	53.6	471	4 US-09-328-352-7581	Sequence 7581, Ap
19	36	52.2	81	4 US-09-489-039A-9928	Sequence 9928, Ap
20	36	52.2	232	2 US-08-869-674-2	Sequence 2, Appli
21	36	52.2	232	4 US-09-213-010-2	Sequence 2, Appli
22	36	52.2	232	4 US-09-213-011-2	Sequence 2, Appli
23	36	52.2	232	4 US-09-583-110-4554	Sequence 4554, Ap
24	36	52.2	282	4 US-09-248-796A-28057	Sequence 28057, A
25	36	52.2	802	4 US-09-889-746-4	Sequence 4, Appli
26	36	52.2	3080	6 5223423-4	Patent No. 5223423
27	35.5	51.4	852	4 US-09-585-858-19	Sequence 19, Appli

28	35.5	51.4	1194	2	US-08-680-326-35	Sequence 35, Appli
29	35	50.7	91	4	US-09-543-681A-6613	Sequence 6613, Ap
30	35	50.7	163	4	US-09-252-991A-29098	Sequence 29098, A
31	35	50.7	213	4	US-09-252-991A-30768	Sequence 30768, A
32	35	50.7	218	3	US-08-875-233-12	Sequence 12, Appli
33	35	50.7	218	3	US-08-875-233-13	Sequence 13, Appli
34	35	50.7	248	4	US-09-270-767-40111	Sequence 40111, A
35	35	50.7	248	4	US-09-270-767-55327	Sequence 55327, A
36	35	50.7	266	4	US-09-252-991A-32512	Sequence 32512, A
37	35	50.7	284	4	US-09-248-796A-19445	Sequence 19445, A
38	35	50.7	499	3	US-09-457-040B-13	Sequence 13, Appli
39	35	50.7	499	4	US-09-905-999-21	Sequence 21, Appli
40	35	50.7	561	4	US-09-812-079A-2	Sequence 2, Appli
41	35	50.7	571	4	US-09-914-259-32	Sequence 32, Appli
42	35	50.7	579	4	US-09-171-699-6	Sequence 6, Appli
43	35	50.7	579	4	US-09-171-699-8	Sequence 8, Appli
44	35	50.7	631	1	US-08-605-541B-12	Sequence 12, Appli
45	35	50.7	752	4	US-09-919-039-235	Sequence 235, App

ALIGNMENTS

RESULT 1
5422259-2
; Patent No. 5422259
; APPLICANT: DE BOTH, MICHEL, BEN TAHAR, SOPHIA, NOEL, MARIANNE;
; PERRET, JOEL
; TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE
; SPECIES CUCUMIS MELO
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/27,563
; FILING DATE: 05-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,255
; FILING DATE: 13-AUG-1990
; SEQ ID NO: 2:
; LENGTH: 217
5422259-2

Query Match 100.0%; Score 69; DB 6; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 2
US-08-398-209-2
; Sequence 2, Application US/08398209
; Patent No. 5789656
; GENERAL INFORMATION:
; APPLICANT: Deboth, Michiel
; APPLICANT: No. 5789656L, Marianne
; APPLICANT: Ben Tahar, Sophia
; APPLICANT: Perret, Joel
; TITLE OF INVENTION: Transgenic Plants Belonging to the
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5789656west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,209
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,563
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/566,255
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 8910848
FILING DATE: 11-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A.
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.21US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-398-209-2

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
DB 1 MDKSESTSAGRNR 14

RESULT 3
US-08-398-209-4
Sequence 4, Application US/08398209
Patent No. 5789656
GENERAL INFORMATION:
APPLICANT: Deboth, Michiel
APPLICANT: No. 57896561, Marianne
APPLICANT: Ben Tahar, Sophia
APPLICANT: Perret, Joel
TITLE OF INVENTION: Transgenic Plants Belonging to the
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5789656west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,209
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,563
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/566,255
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 8910848
FILING DATE: 11-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A.
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.21US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-398-209-4

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
DB 1 MDKSESTSAGRNR 14

RESULT 4
US-08-553-619B-3
Sequence 3, Application US/08553619B
Patent No. 5919705
GENERAL INFORMATION:
APPLICANT: Dehaan, Petrus T.
TITLE OF INVENTION: Virus Resistant Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5919705artis Crop Protection
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,619B
FILING DATE: December 1, 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 137-1082/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/354-3588
TELEFAX: 415/857-1125
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-619B-3

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
DB 1 MDKSESTSAGRNR 14

```
RESULT 5
US-08-875-233-2
; Sequence 2, Application US/08875233
; Patent No. 6127601
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell
; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; CUCUMBER MOSAIC VIRUS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-233-2

Query Match      100.0%; Score 69; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDKSESTSAGRNR 14
Db      1 MDKSESTSAGRNR 14

RESULT 6
US-08-875-233-4
; Sequence 4, Application US/08875233
; Patent No. 6127601
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell
; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; CUCUMBER MOSAIC VIRUS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-233-4

Query Match      100.0%; Score 69; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDKSESTSAGRNR 14
Db      1 MDKSESTSAGRNR 14
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-233-4

Query Match      100.0%; Score 69; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDKSESTSAGRNR 14
Db      1 MDKSESTSAGRNR 14

RESULT 7
US-08-875-233-6
; Sequence 6, Application US/08875233
; Patent No. 6127601
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell
; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; CUCUMBER MOSAIC VIRUS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-233-6

Query Match      100.0%; Score 69; DB 3; Length 218;
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Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 8

US-08-875-233-15
; Sequence 15, Application US/08875233
; Patent No. 6127601

; GENERAL INFORMATION:

; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell
; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; TITLE OF INVENTION: Cucumber Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Rockey, Milanow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997

; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460

; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; US-08-875-233-15

Query Match 100.0%; Score 69; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 9

US-09-127-742-2
; Sequence 2, Application US/09127742A
; Patent No. 6198022

; GENERAL INFORMATION:

; APPLICANT: DE BOTH, MICHAEL
; APPLICANT: NOEL, MARIANNE
; APPLICANT: TAHAR, SOPHIA BEN
; APPLICANT: PERRET, JOEL
; APPLICANT: BIOSEM

; TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE SPECIES CUCUMIS MELO
; FILE REFERENCE: 8076.21USD2
; CURRENT APPLICATION NUMBER: US/09/127,742A
; CURRENT FILING DATE: 1998-08-03

; EARLIER APPLICATION NUMBER: 08/398,209
; EARLIER FILING DATE: 1995-03-02

; EARLIER APPLICATION NUMBER: 08/027,563

; EARLIER FILING DATE: 1993-03-05

; EARLIER APPLICATION NUMBER: 07/566,255

; EARLIER FILING DATE: 1990-08-13

; EARLIER APPLICATION NUMBER: FR 89 10848

; EARLIER FILING DATE: 1989-08-11

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 2

; LENGTH: 218

; TYPE: PRT

; ORGANISM: cucumber mosaic virus

US-09-127-742-2

Query Match 100.0%; Score 69; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 10

US-09-127-742-4
; Sequence 4, Application US/09127742A
; Patent No. 6198022

; GENERAL INFORMATION:

; APPLICANT: DE BOTH, MICHAEL
; APPLICANT: NOEL, MARIANNE
; APPLICANT: TAHAR, SOPHIA BEN
; APPLICANT: PERRET, JOEL
; APPLICANT: BIOSEM

; TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE SPECIES CUCUMIS MELO
; FILE REFERENCE: 8076.21USD2

; CURRENT APPLICATION NUMBER: US/09/127,742A

; CURRENT FILING DATE: 1998-08-03

; EARLIER APPLICATION NUMBER: 08/398,209

; EARLIER FILING DATE: 1995-03-02

; EARLIER APPLICATION NUMBER: 08/027,563

; EARLIER FILING DATE: 1993-03-05

; EARLIER APPLICATION NUMBER: 07/566,255

; EARLIER FILING DATE: 1990-08-13

; EARLIER APPLICATION NUMBER: FR 89 10848

; EARLIER FILING DATE: 1989-08-11

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 4

; LENGTH: 218

; TYPE: PRT

; ORGANISM: cucumber mosaic virus

US-09-127-742-4

Query Match 100.0%; Score 69; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 11

5422259-4
; Patent No. 5422259

; APPLICANT: DE BOTH, MICHAEL, BEN TAHAR, SOPHIA, NOEL, MARIANNE;
; PERRET, JOEL

; TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE
; SPECIES CUCUMIS MELO

; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/27,563
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 566,255
FILING DATE: 13-AUG-1990
SEQ ID NO:4:
LENGTH: 218
5422259-4

Query Match 100.0%; Score 69; DB 6; length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 12

US-08-875-233-10
Sequence 10, Application US/08875233
Patent No. 6127601

GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-10

Query Match 92.8%; Score 64; DB 3; length 218;
Best Local Similarity 92.9%; Pred. No. 0.0009;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 13

US-09-513-999C-4827
Sequence 4827, Application US/09513999C
Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4827
LENGTH: 64
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-4827

Query Match 56.5%; Score 39; DB 4; length 64;
Best Local Similarity 58.3%; Pred. No. 6.6;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 KSESTSAGRNR 14
Db 53 QSESTNGKNKR 64

RESULT 14

US-08-961-564A-5
Sequence 5, Application US/08961564A
Patent No. 6114515

GENERAL INFORMATION:

APPLICANT: WU, SHUIJIAN
APPLICANT: SWEET, RAYMOND
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: PIGRL-1, A MEMBER OF IMMUNOGLOBULIN
TITLE OF INVENTION: GENE SUPERFAMILY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,564A
FILING DATE: 30-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/056,935
FILING DATE: 25-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70236
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-961-564A-5

Query Match 56.5%; Score 39; DB 3; Length 66;
Best Local Similarity 72.7%; Pred. No. 6.8;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DKSESTSGRNR 12
|||:|||||
Db 27 DK1ETKSAGRNR 37

RESULT 15

US-09-382-080-3

; Sequence 3, Application US/09382080

; Patent No. 6087333

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Goli, Surya K.

; TITLE OF INVENTION: DISEASE ASSOCIATED ACIDIC PROTEIN

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/382,080

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/859,937

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0308 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 172 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 1276649

; US-09-382-080-3

Query Match 55.1%; Score 38; DB 3; Length 172;

Best Local Similarity 70.0%; Pred. No. 29;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 ESTSAGRNR 14
:|:|||||
Db 87 DSTMSGNRNR 96

Search completed: December 5, 2004, 08:07:56
Job time : 24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 5, 2004, 08:04:17 ; Search time 353 Seconds
(without alignments)
14.144 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSGRNRR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	218	US-10-011-033-2	Sequence 2, Appli
2	69	100.0	218	US-10-011-033-4	Sequence 6, Appli
3	69	100.0	218	US-10-011-033-6	Sequence 15, Appli
4	69	100.0	218	US-10-011-033-15	Sequence 10, Appli
5	64	92.8	218	US-10-011-033-10	Sequence 189118,
6	43	62.3	225	US-10-437-963-189118	Sequence 135827,
7	41	59.4	193	US-10-437-963-135827	Sequence 150193,
8	41	59.4	254	US-10-437-963-150193	Sequence 190100,
9	41	59.4	273	US-10-437-963-190100	Sequence 184959,
10	40	58.0	159	US-10-424-599-184959	Sequence 190976,
11	40	58.0	202	US-10-425-115-190976	Sequence 31499, A
12	39	56.5	68	US-10-029-386-31499	Sequence 188688,
13	39	56.5	103	US-10-425-115-188688	

14	39	56.5	1104	14	US-10-369-493-4135	Sequence 4135, App
15	38	55.1	109	17	US-10-425-115-253470	Sequence 253470, App
16	38	55.1	121	17	US-10-425-115-249986	Sequence 249986, App
17	38	55.1	197	15	US-10-452-858C-31	Sequence 31, Appl
18	38	55.1	251	16	US-10-437-963-109979	Sequence 109979, App
19	38	55.1	319	14	US-10-156-761-11072	Sequence 11072, App
20	38	55.1	371	15	US-10-425-114-50396	Sequence 50396, App
21	38	55.1	420	17	US-10-425-115-357819	Sequence 357819, App
22	38	55.1	493	15	US-10-425-114-63801	Sequence 63801, App
23	38	55.1	493	17	US-10-425-115-201525	Sequence 201525, App
24	38	55.1	530	16	US-10-437-963-193875	Sequence 193875, App
25	38	55.1	703	15	US-10-424-599-247762	Sequence 247762, App
26	38	55.1	1511	14	US-10-369-493-22496	Sequence 22496, App
27	38	55.1	19662	15	US-10-084-846A-6	Sequence 6, Appli
28	37	53.6	89	16	US-10-437-963-151781	Sequence 151781, App
29	37	53.6	113	14	US-10-266-886-7	Sequence 7, Appli
30	37	53.6	142	16	US-10-437-963-110739	Sequence 110739, App
31	37	53.6	147	16	US-10-767-701-56363	Sequence 56363, App
32	37	53.6	183	15	US-10-425-114-51049	Sequence 51049, App
33	37	53.6	198	16	US-10-437-963-129622	Sequence 129622, App
34	37	53.6	202	16	US-10-437-963-110737	Sequence 110737, App
35	37	53.6	205	15	US-10-424-599-215773	Sequence 215773, App
36	37	53.6	223	9	US-09-925-300-1246	Sequence 1246, App
37	37	53.6	265	9	US-09-925-302-559	Sequence 559, App
38	37	53.6	265	10	US-09-925-302-559	Sequence 559, App
39	37	53.6	275	15	US-10-282-122A-49014	Sequence 49014, App
40	37	53.6	276	15	US-10-374-780A-1883	Sequence 1883, App
41	37	53.6	277	14	US-10-369-493-4258	Sequence 4258, App
42	37	53.6	281	16	US-10-437-963-136159	Sequence 136159, App
43	37	53.6	375	17	US-10-425-115-323368	Sequence 323368, App
44	37	53.6	448	16	US-10-437-963-169865	Sequence 169865, App
45	37	53.6	672	14	US-10-291-265-455	Sequence 455, App

ALIGNMENTS

RESULT 1
US-10-011-033-2
; Sequence 2, Application US/10011033
; Publication No. US20020124286A1
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; McMaster, J. Russell
; Tricoll, David M
; Reynolds, John F
; Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; Cucurbit Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011, 033
; FILING DATE: 13-No. US20020124286A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/875, 233
; FILING DATE: 26-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-011-033-2

Query Match 100.0%; Score 69; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 2

US-10-011-033-4
; Sequence 4, Application US/10011033
; Publication No. US20020124286A1
; GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.

STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,033

FILING DATE: 13-No. US20020124286A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/875,233

FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lisa V. Mueller

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 218 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-011-033-4

Query Match 100.0%; Score 69; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 3

US-10-011-033-6
; Sequence 6, Application US/10011033
; Publication No. US20020124286A1
; GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.

STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,033

FILING DATE: 13-No. US20020124286A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/875,233

FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lisa V. Mueller

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 218 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-011-033-6

Query Match 100.0%; Score 69; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 4

US-10-011-033-15
; Sequence 15, Application US/10011033
; Publication No. US20020124286A1
; GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L

McMaster, J. Russell

Tricoli, David M

Reynolds, John F

Carney, Kim J

TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.

STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700

CITY: Chicago

CITY: Chicago

STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-011-033-15

Query Match 100.0%; Score 69; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 5
US-10-011-033-10
Sequence 10, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-011-033-10

Query Match 92.8%; Score 64; DB 13; Length 218;
Best Local Similarity 92.9%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 6
US-10-437-963-189118
Sequence 189118, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 189118
LENGTH: 225
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_85657C.1.pep
US-10-437-963-189118

Query Match 62.3%; Score 43; DB 16; Length 225;
Best Local Similarity 57.1%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 19 MSNSDKTTAGRHRR 32

RESULT 7
US-10-437-963-135827
Sequence 135827, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963


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/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 135827
/ LENGTH: 193
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_37465C.1.pep
US-10-437-963-135827
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Query Match          59.4%; Score 41; DB 16; Length 193;
Best Local Similarity 66.7%; Pred. No. 50;
Matches      8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY      1 MDKSESTSAGRNR 12
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Db      1 MDPSEETSAGKD 12
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RESULT 8

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US-10-437-963-150193
/ Sequence 150193, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 150193
/ LENGTH: 254
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_50452C.1.pep
US-10-437-963-150193
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Query Match          59.4%; Score 41; DB 16; Length 254;
Best Local Similarity 50.0%; Pred. No. 67;
Matches      7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
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QY      1 MDKSESTSAGRNR 14
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Db      140 LEKSKSTRNGKNKR 153
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RESULT 9

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US-10-437-963-190100
/ Sequence 190100, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
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/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 190100
/ LENGTH: 273
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_86546C.1.pep
US-10-437-963-190100
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Query Match          59.4%; Score 41; DB 16; Length 273;
Best Local Similarity 69.2%; Pred. No. 72;
Matches      9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY      2 DKSESTSAGRNR 14
      |||:|||||:
Db      203 DWSESSSNGENRR 215
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RESULT 10

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US-10-424-599-184959
/ Sequence 184959, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 184959
/ LENGTH: 159
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_138032C.1.pep
US-10-424-599-184959
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Query Match          58.0%; Score 40; DB 15; Length 159;
Best Local Similarity 88.9%; Pred. No. 62;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      6 STSAGRNR 14
      |||||:||||
Db      2 STSAGQNR 10
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RESULT 11

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US-10-425-115-190976
/ Sequence 190976, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 190976
/ LENGTH: 202
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_105749C.1.pep
US-10-425-115-190976
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Query Match 58.0%; Score 40; DB 17; length 202;
Best Local Similarity 53.8%; Pred. No. 79;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 DKSESTSAGRNR 14
|:|:|:|:|:|:|
Db 31 DRSEASAPGRGR 43

RESULT 12

US-10-029-386-31499
; Sequence 31499, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31499
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC020728.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
; OTHER INFORMATION: SWISSPROT HIT: P42285, EVALUATE 2.00e-20
US-10-029-386-31499

Query Match 56.5%; Score 39; DB 14; length 68;
Best Local Similarity 58.3%; Pred. No. 39;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 KSESTSAGRNR 14
:|:|:|:|:|:|
Db 31 QSESTNNGKNR 42

RESULT 13

US-10-425-115-188688
; Sequence 188688, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 188688
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_103673C.1.pep
US-10-425-115-188688

Query Match 56.5%; Score 39; DB 17; length 103;
Best Local Similarity 50.0%; Pred. No. 59;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 MDKSESTSAGRNR 14
:|:|:|:|:|:|
Db 85 LDQLSXTMSGNR 98

RESULT 14

US-10-369-493-4135
; Sequence 4135, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4135
; LENGTH: 1104
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-4135

Query Match 56.5%; Score 39; DB 14; length 1104;
Best Local Similarity 53.8%; Pred. No. 6.6e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 DKSESTSAGRNR 14
||:|:|:|:|:|
Db 985 DKTEKRAAGRNTK 997

RESULT 15

US-10-425-115-253470
; Sequence 253470, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 253470
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_162747C.1.pep
US-10-425-115-253470

Query Match 55.1%; Score 38; DB 17; length 109;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 KSESTSAGRNR 14
|:|:|:|:|:|:|
Db 90 KKTTTAAKNRK 101

Search completed: December 5, 2004, 08:13:54

Job time : 353 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 06:06:43 ; Search time 1421 Seconds
(without alignments)
1763.796 Million cell updates/sec

Title: US-09-857-841-3
Perfect score: 53
Sequence: 1 gatccatgcacaatctgaa.....gtcgtaccgtcgacgagct 53

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
3: gb_in:*
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6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	53	6	BD261798 Enhanceme
2	46	86.8	771	6	AR111976 Sequence
3	46	86.8	772	6	AR111981 Sequence
4	46	86.8	792	6	AR111975 Sequence
5	45.8	86.4	130	6	AR031575 Sequence
6	45.8	86.4	130	6	AR065687 Sequence
7	45.8	86.4	130	6	AR097446 Sequence
8	45.8	86.4	130	6	I49964 Sequence 14
9	45.8	86.4	131	6	AR031572 Sequence
10	45.8	86.4	131	6	AR065684 Sequence
11	45.8	86.4	131	6	AR097443 Sequence
12	45.8	86.4	131	6	I49961 Sequence 11
13	45.8	86.4	152	6	AR031570 Sequence
14	45.8	86.4	152	6	AR065682 Sequence
15	45.8	86.4	152	6	AR097441 Sequence
16	45.8	86.4	152	6	I49959 Sequence 9
17	45.8	86.4	154	6	AR031574 Sequence
18	45.8	86.4	154	6	AR065686 Sequence
19	45.8	86.4	154	6	AR097445 Sequence

20	45.8	86.4	154	6	I49963 Sequence 13
21	45.8	86.4	862	14	CMU32859 Cucumber mo
22	45.8	86.4	864	14	CMU32858 Cucumber mo
23	45.8	86.4	894	14	MCVCPB L36525 Cucumber mo
24	45.8	86.4	976	6	A32131 CMV capsid
25	45.8	86.4	976	6	AR021486 Sequence
26	45.8	86.4	976	6	AR138342 Sequence
27	45.8	86.4	976	6	AR364710 Sequence
28	45.8	86.4	976	6	BD000278 Transgeni
29	45.8	86.4	1007	6	A32133 CMV capsid
30	45.8	86.4	1007	6	A39812 Sequence 6
31	45.8	86.4	1007	6	AR021487 Sequence
32	45.8	86.4	1007	6	AR138343 Sequence
33	45.8	86.4	1007	6	AR364711 Sequence
34	45.8	86.4	1007	6	AR430190 Sequence
35	45.8	86.4	1007	6	BD000279 Transgeni
36	45.8	86.4	1007	14	CUMCVRN4 X16386 Cucumber mo
37	45.8	86.4	1033	14	CMU22821 U22821 Cucumber mo
38	45.8	86.4	1043	14	CMVCOATP X77855 Cucumber Mo
39	45.8	86.4	1066	6	A67212 Sequence 1
40	45.8	86.4	1067	6	AR076864 Sequence
41	45.8	86.4	1113	14	CMO131624 Cucumber
42	45.8	86.4	1115	14	CMO131623 Cucumber
43	45.8	86.4	1362	14	MCVCPA M22710 Cucumber mo
44	45.8	86.4	1379	6	E01821 cDNA encodi
45	45.8	86.4	1696	6	A41823 Sequence 4

ALIGNMENTS

RESULT 1	BD261798	53 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD261798				
DEFINITION	BD261798	Enhancement in protein production by higher plants using ubiquitin			
ACCESSION	BD261798.1	GI:33071566			
VERSION	JP 2002532098-A/2.				
KEYWORDS	Cucumber mosaic virus (cucumber mosaic cucumovirus)				
SOURCE	Cucumber mosaic virus				
ORGANISM	Cucumovirus.				
REFERENCE	1 (bases 1 to 53)				
AUTHORS	Fang,R.X., Wu,J.L. and Chen,X.Y.				
TITLE	Enhancement in protein production by higher plants using ubiquitin				
JOURNAL	or cucumber mosaic virus coating protein peptide				
COMMENT	Patent: JP 2002532098-A 2 02-OCT-2002;				
	INSTITUTE OF MOLECULAR AGROBIOLOGY				
	OS Cucumber mosaic virus				
	PN JP 2002532098-A/2				
	PD 02-OCT-2002				
	PF 11-DEC-1998 JP 2000588378				
	PI RONG XIANG FANG,JUNG LIN WU,XIAO YING CHEN				
	PC C12N15/09,A01H5/00,C07K14/415,C07K19/00,C12N5/10,C12N15/00, PC				
	C12N5/00				
	CC Enhancement in protein production by higher plants using				
	CC ubiquitin or				
	CC cucumber mosaic virus coating protein peptide FH				Key
FEATURES	Location/Qualifiers				
Source	1..53				
	/organism="Cucumber mosaic virus"				
	/mol_type="Genomic DNA"				
	/db_xref="taxon:12305"				
ORIGIN					
Query Match	100.0%;	Score 53;	DB 6;	Length 53;	
Best Local Similarity	100.0%;	Pred. No. 3.6e-11;			
Matches	53;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GATCCATGACAATCTGAATCAACCACTGCTGCTGTAACCGTCGACGAGCT	53		

Db 1 GATCCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACGAGCT 53

RESULT 2
AR111976
LOCUS AR111976 771 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6127601.
ACCESSION AR111976
VERSION AR111976.1 GI:12828824
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 771)
Boeshore,M.L., McMaster,R.J., Tricoli,D.M., Reynolds,J.F. and
Carney,K.J.
TITLE Plants resistant to C strains of cucumber mosaic virus
JOURNAL Patent: US 6127601-A 5 03-OCT-2000;
FEATURES location/Qualifiers
SOURCE 1..771
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 86.8%; Score 46; DB 6; Length 771;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
1 CCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46

RESULT 3
AR111981
LOCUS AR111981 772 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 14 from patent US 6127601.
ACCESSION AR111981
VERSION AR111981.1 GI:12828829
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 772)
Boeshore,M.L., McMaster,R.J., Tricoli,D.M., Reynolds,J.F. and
Carney,K.J.
TITLE Plants resistant to C strains of cucumber mosaic virus
JOURNAL Patent: US 6127601-A 14 03-OCT-2000;
FEATURES location/Qualifiers
SOURCE 1..772
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 86.8%; Score 46; DB 6; Length 772;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
1 CCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46

RESULT 4
AR111975
LOCUS AR111975 792 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6127601.
ACCESSION AR111975
VERSION AR111975.1 GI:12828823
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 792)
Boeshore,M.L., McMaster,R.J., Tricoli,D.M., Reynolds,J.F. and
Carney,K.J.
TITLE Plants resistant to C strains of cucumber mosaic virus
JOURNAL Patent: US 6127601-A 3 03-OCT-2000;
FEATURES location/Qualifiers
SOURCE 1..792
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 86.8%; Score 46; DB 6; Length 792;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
1 CCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46

RESULT 5
AR031575
LOCUS AR031575 130 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5866384.
ACCESSION AR031575
VERSION AR031575.1 GI:5945864
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 130)
Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 14 02-FEB-1999;
FEATURES location/Qualifiers
SOURCE 1..130
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 86.4%; Score 45.8; DB 6; Length 130;
Best Local Similarity 95.9%; Pred. No. 4.6e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATCCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
48 GAGTCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 6
AR065687
LOCUS AR065687 130 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5849548.
ACCESSION AR065687
VERSION AR065687.1 GI:5995903
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 130)
Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 14 15-DEC-1998;
FEATURES location/Qualifiers
SOURCE 1..130
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 86.4%; Score 45.8; DB 6; Length 130;
Best Local Similarity 95.9%; Pred. No. 4.6e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||
48 GAGTCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

Db

RESULT 7
AR097446 130 bp DNA linear PAT 14-FEB-2001
LOCUS AR097446
DEFINITION Sequence 14 from patent US 6071730.
ACCESSION AR097446
VERSION AR097446.1 GI:12806176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 14 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..130
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 86.4%; Score 45.8; DB 6; Length 130;
Best Local Similarity 95.9%; Pred. No. 4.6e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||
48 GAGTCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

Db

RESULT 8
I49964 130 bp DNA linear PAT 07-OCT-1997
LOCUS I49964
DEFINITION Sequence 14 from patent US 5641673.
ACCESSION I49964
VERSION I49964.1 GI:2472184
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5641673-A 14 24-JUN-1997;
FEATURES Location/Qualifiers
source 1..130
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 86.4%; Score 45.8; DB 6; Length 130;
Best Local Similarity 95.9%; Pred. No. 4.6e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||
48 GAGTCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

Db

RESULT 9
AR031572 131 bp DNA linear PAT 29-SEP-1999
LOCUS AR031572
DEFINITION Sequence 11 from patent US 5866384.
ACCESSION AR031572
VERSION AR031572.1 GI:5945861
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 11 02-FEB-1999;
FEATURES Location/Qualifiers
source 1..131
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 86.4%; Score 45.8; DB 6; Length 131;
Best Local Similarity 95.9%; Pred. No. 4.6e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||
49 GAGTCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 97

Db

RESULT 10
AR065684 131 bp DNA linear PAT 29-SEP-1999
LOCUS AR065684
DEFINITION Sequence 11 from patent US 5849548.
ACCESSION AR065684
VERSION AR065684.1 GI:5995900
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 11 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..131
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 86.4%; Score 45.8; DB 6; Length 131;
Best Local Similarity 95.9%; Pred. No. 4.6e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||
49 GAGTCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 97

Db

RESULT 11
AR097443 131 bp DNA linear PAT 14-FEB-2001
LOCUS AR097443
DEFINITION Sequence 11 from patent US 6071730.
ACCESSION AR097443
VERSION AR097443.1 GI:12806173
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 11 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..131
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 86.4%; Score 45.8; DB 6; Length 131;
Best Local Similarity 95.9%; Pred. No. 4.6e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 49
|||
49 GAGTCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 97

Db

RESULT 12

LOCUS I49961 131 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 11 from patent US 5641673.

ACCESSION I49961

VERSION I49961.1 GI:2472181

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

1 (bases 1 to 131)

AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.

TITLE Cell ablation using trans-splicing ribozymes

JOURNAL Patent: US 5641673-A 11 24-JUN-1997;

FEATURES Location/Qualifiers

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/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 86.4%; Score 45.8; DB 6; Length 131;

Best Local Similarity 95.9%; Pred.No.4.6e-08;

Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 49
|||
49 GAGTCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 97

Db

RESULT 13

LOCUS AR031570 152 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 9 from patent US 5866384.

ACCESSION AR031570

VERSION AR031570.1 GI:5945859

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

1 (bases 1 to 152)

AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.

TITLE Cell ablation using trans-splicing ribozymes

JOURNAL Patent: US 5866384-A 9 02-FEB-1999;

FEATURES Location/Qualifiers

source 1..152

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 86.4%; Score 45.8; DB 6; Length 152;

Best Local Similarity 95.9%; Pred.No.4.7e-08;

Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 49
|||
70 GAGTCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 118

Db

RESULT 14

LOCUS AR065682 152 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 9 from patent US 5849548.

ACCESSION AR065682

VERSION AR065682.1 GI:5995898

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

REFERENCE 1 (bases 1 to 152)

AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.

TITLE Cell ablation using trans-splicing ribozymes

JOURNAL Patent: US 5849548-A 9 15-DEC-1998;

FEATURES Location/Qualifiers

source 1..152

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 86.4%; Score 45.8; DB 6; Length 152;

Best Local Similarity 95.9%; Pred.No.4.7e-08;

Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 49
|||
70 GAGTCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 118

Db

RESULT 15

LOCUS AR097441 152 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 9 from patent US 6071730.

ACCESSION AR097441

VERSION AR097441.1 GI:12806171

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

1 (bases 1 to 152)

AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.

TITLE Cell ablation using trans-splicing ribozymes

JOURNAL Patent: US 6071730-A 9 06-JUN-2000;

FEATURES Location/Qualifiers

source 1..152

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 86.4%; Score 45.8; DB 6; Length 152;

Best Local Similarity 95.9%; Pred.No.4.7e-08;

Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 49
|||
70 GAGTCATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGACG 118

Db

Search completed: December 5, 2004, 07:02:45

Job time : 1423 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 03:32:53 ; Search time 224 Seconds
(without alignments)
1242.051 Million cell updates/sec

Title: US-09-857-841-3

Perfect score: 53

Sequence: 1 gatccatgacaatctgaa.....gtcgtaccgctgcagagct 53

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Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	53	3	AAA30858 Ubiquitin
2	46	86.8	771	2	AAT34666 Coat prot
3	46	86.8	773	2	AAT34665 Coat prot
4	45.8	86.4	976	2	AAQ10461 Capsid pr
5	45.8	86.4	1007	2	AAQ10462 Capsid pr
6	45.8	86.4	1007	2	AAQ67395 Cauliflow
7	45.8	86.4	1066	2	AAT99545 Cucumber
8	45.8	86.4	1067	2	AAZ07505 Cucumber
9	45.8	86.4	1379	1	AAN81111 Sequence
10	45.8	86.4	1696	2	AAQ76107 Cucumber
11	45.8	86.4	1860	2	AAQ76106 Cucumber
12	45.8	86.4	2173	2	AAQ76108 Cucumber
13	44.4	83.8	772	2	AAT34664 Coat prot
14	44.4	83.8	772	2	AAT17259 Coat prot
15	44.2	83.4	1423	1	AAN90249 Cucumber
16	44.2	83.4	1423	2	AAT72272 Cucumber
17	42.6	80.4	894	3	ABL58209 Agrobacte
18	42.4	80.0	657	2	AAQ03641 Cucumber
19	26.4	49.8	657	2	AAQ41742 Cucumber
20	26.4	49.8	657	2	AAQ80683 CMV-SA co
21	24.8	46.8	657	2	AAQ03640 Cucumber

C	22	24	45.3	1068	2	AAV52506	Aav52506 Streptoco
	23	23.4	44.2	1990	2	AAQ44294	Aaq44294 Pectin es
	24	22.8	43.0	402	3	AAC46250	Aac46250 Arabidops
	25	22.8	43.0	642	6	ABK33838	Abk33838 Bacillus
	26	22.6	42.6	4385	4	AAS59663	Aas59663 Propionib
	27	22.6	42.6	4385	8	ACF64592	Acf64592 Propionib
C	28	22.6	42.6	31248	9	ACC58250	Acc58250 Coumermyc
	29	22.6	42.6	34720	2	AAV30458_5	Continuation (6 of
	30	22.6	42.6	35359	9	ACC58251	Continuation (6 of
	31	22.6	42.6	36165	2	AAV30459_5	Continuation (6 of
	32	22.4	42.3	1182	5	AAH65738	Aah65738 C glutami
	33	22.4	42.3	1266	4	AAF71669	Aaf71669 Corynebac
	34	22.4	42.3	34980	5	AAH68526	Aah68526 C glutami
	35	22.2	41.9	109	12	ADH51395	Adh51395 Baculovir
C	36	22.2	41.9	480	12	ADM36208	Adm36208 Murine SS
	37	22.2	41.9	691	12	ADM36228	Adm36228 Murine SS
	38	22.2	41.9	1836	12	ADM36206	Adm36206 Murine SS
C	39	22.2	41.9	2638	3	AAC42012	Aac42012 Arabidops
	40	22	41.5	1230	6	ABQ73845	Abq73845 Rhizobium
C	41	22	41.5	3707	2	AAQ82792	Aaq82792 TRK1 gene
	42	22	41.5	3708	5	AAH21448	Aah21448 S. cerevi
C	43	22	41.5	5729	4	AAI66254	Aai66254 S. cerevis
	44	22	41.5	5729	10	ADD02790	Add02790 S. cerevi
	45	21.8	41.1	291	2	AAK60502	Aak60502 WO9914235

ALIGNMENTS

RESULT 1	AAA30858	standard; DNA; 53 BP.
XX	AAA30858	
AC	AAA30858;	
DT	19-SEP-2000	(first entry)
XX		
DE	Ubiquitin monomer C-terminal fragment coding sequence.	
XX		
KW	Ubiquitin monomer; protein production; plant cell; ubiquitin promoter;	
XX	ds.	
OS	Nicotiana tabacum.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	6..47
FT		/*tag= a
FT		/product= "Ubiquitin_monomer_fragment"
XX		
PN	WO200036129-A1.	
XX		
PD	22-JUN-2000.	
XX		
PF	11-DEC-1998;	98WO-SG000103.
XX		
PR	11-DEC-1998;	98WO-SG000103.
XX		
PA	(MOLE-) INST MOLECULAR AGROBIOLOGY.	
XX		
PI	Fang R, Wu J, Chen X;	
XX		
DR	WPI; 2000-431604/37.	
DR	P-PSDB; AAV90255.	
XX		
PT	Production of desired protein in plants or plant cells by linking a	
PT	ubiquitin monomer coding sequence upstream of the gene encoding the	
PT	desired protein.	
XX		
PS	Claim 8; Page 18; 42pp; English.	
XX		
CC	This sequence encodes the C-terminal fragment of a ubiquitin monomer. The	
CC	invention relates to a method for enhancing production of a desired	

CC protein in a plant or plant cell by inserting a nucleic acid (NA)
CC encoding a ubiquitin monomer upstream of a NA encoding the desired
CC protein, where the fusion construct encodes a fusion protein and
CC expression is not controlled by the ubiquitin promoter. The invention
CC also relates to a NA acid vector a NA vector able to transform a plant
CC cell, that comprises NA encoding a fusion protein having a ubiquitin
CC monomer linked to a protein of interest and further, where expression of
CC the fusion construct is not under control of a ubiquitin promoter. The
CC construct allows enhanced production of the desired protein in plants or
CC plant cells
XX
SQ Sequence 53 BP; 15 A; 14 C; 13 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 53; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.9e-11;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATCCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACGAGCT 53
1 GATCCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACGAGCT 53
Db

RESULT 2
AAT34666
ID AAT34666 standard; DNA; 771 BP.
XX
AC AAT34666;

DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)

XX Coat protein of the V34 strain of cucumber mosaic virus.

XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance; ss.
XX
OS Cucumber mosaic virus; strain V34.

XX
FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a

XX
PN WO9621018-A1.
PD 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
DR WPI; 1996-333993/33.
DR P-PSDB; AAR98895.

XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX

PS Claim 24; Fig 3; 80pp; English.

XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX
SQ Sequence 771 BP; 176 A; 199 C; 183 G; 213 T; 0 U; 0 Other;

Query Match 86.8%; Score 46; DB 2; Length 771;

Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
1 CCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46
Db

RESULT 3
AAT34665
ID AAT34665 standard; DNA; 773 BP.
XX
AC AAT34665;

DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)

XX Coat protein of the V33 strain of cucumber mosaic virus.

XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance; ss.
XX
OS Cucumber mosaic virus; strain V33.

XX
FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a

XX
PN WO9621018-A1.
PD 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
DR WPI; 1996-333993/33.
DR P-PSDB; AAR98894.

XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX

PS Claim 13; Fig 2; 80pp; English.

XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX
SQ Sequence 773 BP; 175 A; 200 C; 185 G; 213 T; 0 U; 0 Other;

Query Match 86.8%; Score 46; DB 2; Length 773;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
1 CCATGGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46
Db

RESULT 4
AAQ10461
ID AAQ10461 standard; cDNA; 976 BP.
XX
AC AAQ10461;

XX

DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-APR-1991 (first entry)
XX Capsid protein gene of Cucumber Mosaic Virus strain FNY.
DE
XX
KM CMV; resistance; capsid protein; Cucumis melo; ss.
XX
OS Cucumber mosaic virus.
XX
FH Key Location/Qualifiers
FT CDS 75..731
FT /*tag= a
FT /product= "CMV strain FNY capsid protein"
XX
XX
PN EP412912-A.
XX
XX 13-FEB-1991.
PD
XX
XX 09-AUG-1990; 90EP-00402282.
PF
XX
XX 11-AUG-1989; 89FR-00010848.
PR
XX
PA (BIOC-) BIOCEM SA.
XX
PI Deboth M, Bentahar S, Noel M, Perret J;
XX
XX WPI; 1991-046027/07.
DR P-PSDB; AAR10652.
DR
XX
XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
PT culture on specific medium for new transformed plants etc., esp.
PT resistant to cucumber mosaic virus.
XX
XX
PS Claim 15; Page 17; 44pp; French.
XX
XX The gene was isolated from a plasmid (pUC18) containing DNA complementary
CC to RNA 3 of the virulent strain FNY, isolated in New York on infected
CC melons. The sequence includes a leader sequence, coding region and 3' non
CC -coding region. The leader sequence is the same length as that of the
CC Japanese Y strain of CMV. Transgenic melon plantlets containing the
CC sequence introduced via an Agrobacterium tumefaciens intermediate are
CC cultured as shoots in special media. The transformed melon plants are
CC resistant to CMV. See also AAQ10462. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC AUG-2003 to correct OS field.)
XX
SQ Sequence 976 BP; 224 A; 249 C; 230 G; 273 T; 0 U; 0 Other;
Query Match 86.4%; Score 45.8; DB 2; Length 976;
Best Local Similarity 95.9%; Pred. No. 5.3e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GATCCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||
DB 70 GAGTCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 118
RESULT 5
AAQ10462
ID AAQ10462 standard; DNA; 1007 BP.
XX
XX
AC AAQ10462;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-APR-1991 (first entry)
XX
XX Capsid protein gene of Cucumber Mosaic Virus strain 117F.
DE
XX
XX CMV; resistance; capsid protein; Cucumis melo; ss.
KW
XX
OS Cucumber mosaic virus.

XX
FH Key Location/Qualifiers
FT CDS 54..710
FT /*tag= a
FT /product= "CMV strain 117F capsid protein"
XX
XX
PN EP412912-A.
XX
XX 13-FEB-1991.
PD
XX
XX 09-AUG-1990; 90EP-00402282.
PF
XX
XX 11-AUG-1989; 89FR-00010848.
PR
XX
PA (BIOC-) BIOCEM SA.
XX
XX
PI Deboth M, Bentahar S, Noel M, Perret J;
XX
XX WPI; 1991-046027/07.
DR P-PSDB; AAR10653.
DR
XX
XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
PT culture on specific medium for new transformed plants etc., esp.
PT resistant to cucumber mosaic virus.
XX
XX
PS Claim 16; Page 19; 44pp; French.
XX
XX The gene was isolated from the virulent French strain 117F of CMV. Tomato
CC plantlets at the 2-leaf stage were infected with CMV strain 117F. 15 days
CC post-infection, the virus was purified from the infected leaves and cDNA
CC was synthesised from RNAs 1,2,3 and 4. After purification and selection
CC by standard techniques, cDNA complementary to RNA 4 was found to encode
CC the capsid protein. It was recloned into "Blue scribe" plasmids and
CC sequenced. Transgenic melon plantlets containing the sequence introduced
CC via an Agrobacterium tumefaciens intermediate are cultured as shoots in
CC special media. The transformed melon plants are resistant to CMV. See
CC also AAQ10461. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
CC 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
CC field.)
XX
SQ Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;
Query Match 86.4%; Score 45.8; DB 2; Length 1007;
Best Local Similarity 95.9%; Pred. No. 5.4e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GATCCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
|||
DB 49 GAGTCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 97
RESULT 6
AAQ67395
ID AAQ67395 standard; DNA; 1007 BP.
XX
XX
AC AAQ67395;
XX
DT 25-MAR-2003 (revised)
DT 12-APR-1995 (first entry)
XX
XX Cauliflower mosaic virus capsid protein coding sequence.
DE
XX
XX Cauliflower mosaic virus; CMV; capsid protein; coat protein;
KW polyribozyme; inactivate; inactivation; resistance; crop protection; ss.
XX
XX Cauliflower mosaic virus.
OS
XX
FH Key Location/Qualifiers
FT CDS 54..710
FT /*tag= a
FT /product= "Capsid protein."
XX
XX
PN FR2701960-A1.


```
XX PD 02-SEP-1994.
XX XX
XX PF 26-FEB-1993; 93FR-00002269.
XX XX
XX PR 26-FEB-1993; 93FR-00002269.
XX XX
XX PA (GENE-) GENE SHEARS PTY LTD.
XX PI Lenee P, Perez P, Gruber V, Baudot G, Ollivo C;
XX XX
XX DR WPI; 1994-281767/35.
XX DR P-PSDB; AAR57968.
XX XX
XX PT New polyribozyme contg. several catalytic regions in complementary
XX PT sequence - can inactivate gene for viral capsid protein, esp. for prepn.
XX PT of new virus resistant transgenic plants, also DNA sequence encoding it.
XX XX
XX PS Disclosure; Fig 2; 67pp; French.
XX XX
XX CC The RNA encoding the capsid protein of cauliflower mosaic virus can be
XX CC targeted by a nucleic acid sequence called a "polyribozyme". The
XX CC polyribozyme has endoribonuclease activity and is able to inactivate the
XX CC gene encoding the viral capsid protein. The polyribozyme comprises
XX CC several catalytic regions derived from ribozymes and confers complete
XX CC resistance to virus. See AAQ67391-94. (Updated on 25-MAR-2003 to correct
XX CC PN field.)
XX XX
XX SQ Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;
XX XX
XX Query Match 86.4%; Score 45.8; DB 2; Length 1007;
XX Best Local Similarity 95.9%; Pred. No. 5.4e-08;
XX Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX XX
OY 1 GATCCATGACAAATCTGAATCAACCGTCTGTCGTAACCGTCGACG 49
Db 49 GAGTCATGACAAATCTGAATCAACCGTCTGTCGTAACCGTCGACG 97
XX XX
RESULT 7
AAT99545/c
ID AAT99545 standard; cDNA; 1066 BP.
XX XX
XX AC AAT99545;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 21-MAY-1998 (first entry)
XX XX
XX DE Cucumber mosaic virus RNA-3 cDNA fragment.
XX XX
XX KW Transgenic plant; virus resistance; disease resistance; RNA virus; CMV;
XX KW coat protein; antisense gene; ss.
XX XX
XX OS Cucumber mosaic virus.
XX XX
XX XX Key Location/Qualifiers
XX FH 3'UTR 1..299
XX FT /*tag= a
XX FT CDS 300..958
XX FT /*tag= b
XX FT /*product= "coat protein"
XX FT sig_peptide 956..1029
XX FT /*tag= c
XX FT /note= "coat protein leader sequence"
XX FT promoter 1030..1066
XX FT /*tag= d
XX FT /note= "F sequence of sub-genomic promoter"
XX XX
XX PN EP806481-A2.
XX XX
XX PD 12-NOV-1997.
XX XX
XX PF 07-MAY-1997; 97EP-00201379.
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XX XX
XX PR 09-MAY-1996; 96IT-MI000927.
XX XX
XX PA (META-) METAPONTUM AGROBIOS SCRL.
XX XX
XX PI Cellini F, Grieco PD;
XX XX
XX DR WPI; 1997-538620/50.
XX XX
XX XX PT Preparing transgenic plants resistant to RNA virus infection - using
XX PT anti:sense gene constructs containing the viral coat protein gene, e.g.
XX PT from cucumber mosaic virus.
XX XX
XX PS Claim 3; Page 10; 18pp; English.
XX XX
XX CC This cDNA clone of cucumber mosaic virus (CMV) RNA-3 includes domain F of
XX CC the subgenomic promoter of viral RNA, the coat protein gene, its leader
XX CC sequence, and the tRNA-like 3'-terminal region of RNA-3. It was prepared
XX CC by amplifying a fragment of CMV cDNA-3 from clone PCR-CMV1RNA3 by PCR
XX CC (see also AAT99548-49). The gene construct is introduced into a vector
XX CC containing a promoter active in plant cells in antisense orientation
XX CC relative to the promoter. A claimed recombinant vector comprises the
XX CC plant promoter, the antisense gene construct and a terminator which is
XX CC functional in the plant. In addition to CMV, viral RNA may also be used
XX CC from tobacco mosaic virus and potato virus. Claimed transgenic plants
XX CC have the antisense gene construct integrated into their genomes. They are
XX CC resistant to viral infection. In particular, they are resistant to CMV.
XX CC Within the antisense gene construct, the interfering activity of the
XX CC antisense F domain of the sub-genomic promoter, associated with the
XX CC antisense activity performed by the coat protein gene, allows production
XX CC of plants having 100% resistance to CMV. (Updated on 25-MAR-2003 to
XX CC correct PR field.)
XX XX
XX SQ Sequence 1066 BP; 299 A; 251 C; 273 G; 243 T; 0 U; 0 Other;
XX XX
XX Query Match 86.4%; Score 45.8; DB 2; Length 1066;
XX Best Local Similarity 95.9%; Pred. No. 5.4e-08;
XX Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX XX
OY 1 GATCCATGACAAATCTGAATCAACCGTCTGTCGTAACCGTCGACG 49
Db 961 GAGTCATGACAAATCTGAATCAACCGTCTGTCGTAACCGTCGACG 913
XX XX
RESULT 8
AAZ07505/c
ID AAZ07505 standard; cDNA; 1067 BP.
XX XX
XX AC AAZ07505;
XX XX
XX DT 26-NOV-1999 (first entry)
XX DT 26-NOV-1999 (first entry)
XX XX
XX DE Cucumber mosaic virus (CMV) RNA-3 gene cDNA clone fragment.
XX XX
XX KW Transgenic plant; RNA virus; antisense construct; cucumber mosaic virus;
XX KW CMV; promoter; coat protein gene; infection; RNA-3; ss.
XX XX
XX OS Cucumber mosaic virus.
XX XX
XX PN US5959181-A.
XX XX
XX PD 28-SEP-1999.
XX XX
XX PF 09-MAY-1997; 97US-00854170.
XX PF 09-MAY-1997; 96IT-MI000927.
XX XX
XX PR 09-MAY-1996; 96IT-MI000927.
XX XX
XX PA (META-) METAPONTUM AGROBIOS SCRL.
XX XX
XX PI Cellini F, Grieco PD;
XX XX
XX DR WPI; 1997-538620/50.
XX XX
```

PT Preparing transgenic plants resistant to RNA virus infection - using
PT anti:sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
PS Claim 2; Fig 1; 15pp; English.
XX
CC The invention relates to preparing transgenic plants resistant to RNA
CC virus induced infections that comprises integrating an antisense gene
CC construct into the plant genome. The construct comprises: (a) an F domain
CC of a subgenomic promoter of cucumber mosaic virus (CMV); (b) downstream
CC from the subgenomic promoter, a leader sequence of a coat protein gene of
CC CMV; (c) downstream from the leader sequence, a gene encoding a CMV coat
CC protein; and (d) downstream from the gene, a 3'-terminal region of a CMV
CC coat protein gene. The method is useful for producing plants which are
CC resistant to infection by RNA based viruses. The gene construct gives
CC higher levels of resistance compared to antisense constructs which are
CC capable of complementing with different domains of genomic RNA of CMV.
CC The present sequence represents the fragment of cDNA clone of RNA-3 of
CC CMV. This forms the antisense construct of the invention

XX SQ Sequence 1067 BP; 297 A; 250 C; 276 G; 244 T; 0 U; 0 Other;

Query Match 86.4%; Score 45.8; DB 2; Length 1067;
Best Local Similarity 95.9%; Pred. No. 5.4e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GATCCATGGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 49
|||
Db 961 GAGTCATGGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 913

RESULT 9
AAN81111
ID AAN81111 standard; DNA; 1379 BP.

XX AC AAN81111;

DT 25-MAR-2003 (revised)
DT 12-NOV-1990 (first entry)

XX DB Sequence contg. CMV strain Y coat protein gene.

XX KM Cucumber mosaic virus; plant viral resistance; ss.

XX OS Synthetic.

FH Key Location/Qualifiers
FT CDS 418..1074
FT /*tag= a
FT /label= cucumber mosaic virus-Y coat protein.

XX PN EP279433-A.

XX PD 24-AUG-1988.

XX PF 18-FEB-1988; 88EP-00102322.

XX PR 20-FEB-1987; 87JP-00038288.

XX PR 25-FEB-1987; 87JP-00043443.

XX PR 18-FEB-1988; 88JP-00035809.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Furusawa I, Onda H, Komiya T;

XX DR WPI; 1988-236708/34.

XX DR P-PSDB; AAP80509.

XX PT DNA coding for the coat protein of cucumber mosaic virus strain Y - used
XX for producing plants resistant to cucumber mosaic virus infection.
XX Disclosure; Page 7; 20pp; English.

CC This DNA is produced on screening of a plasmid library and is used to
CC transform plant cells which subsequently produce the coat prot- ein of
CC cucumber mosaic virus (CMV) strain Y. This protein is not synthesised in
CC natural plant cells. The resistance to CMV infect- ion, provided by the
CC DNA, is shown in plant cells and redifferent- lated plant bodies. See
CC also AAN81110. (Updated on 25-MAR-2003 to correct PR field.) (Updated on
CC 25-MAR-2003 to correct PA field.)

XX SQ Sequence 1379 BP; 306 A; 342 C; 333 G; 398 T; 0 U; 0 Other;

Query Match 86.4%; Score 45.8; DB 1; Length 1379;
Best Local Similarity 95.9%; Pred. No. 5.7e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GATCCATGGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 49
|||
Db 413 GAGTCATGGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 461

RESULT 10

AAQ76107
ID AAQ76107 standard; DNA; 1696 BP.

XX AC AAQ76107;

DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)

XX DE Cucumber mosaic virus RNA-3 chimera encoding RNase T1.

XX KM Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
XX virus resistance; disease resistance; transgenic plant; cross protection;
XX hypersensitive response; crop improvement; tomato;
XX Lycopersicon esculentum; tobacco; Nicotiana tabacum; RNase T1;
XX cell inhibitory protein; ToMV; CMV; ss.

XX OS Cucumber mosaic virus.

FH Key Location/Qualifiers
FT CDS 123..437
FT /*tag= a
FT /product= "RNase T1"

XX PN WO9429464-A1.

XX PD 22-DEC-1994.

XX PF 03-JUN-1994; 94WO-EP001817.

XX PR 04-JUN-1993; 93GB-00011593.

XX PA (SANO) SANDOZ LTD.

XX PA (SANO) SANDOZ PATENT GMBH.

XX PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX PI De Haan PT;

XX DR WPI; 1995-036490/05.

XX DR P-PSDB; AAR67754.

XX PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
XX encodes RNA that interacts with viral RNA polymerase to generate an
XX eliciting agent.

XX PS Claim 4; Page 31-32; 50pp; English.

XX CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76107) has the coat
XX protein gene replaced by a gene encoding a cell inhibitory protein, RNase
XX T1, having the sequence given in AAR67754. The construct elicits a minus-
XX sense RNA that interacts with the RNA-dependent RNA-polymerase of an
XX invading virus, thus conferring virus-resistance on a host plant, e.g.
XX tobacco, tomato. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 1696 BP; 387 A; 413 C; 389 G; 507 T; 0 U; 0 Other;
Query Match 86.4%; Score 45.8; DB 2; Length 1696;
Best Local Similarity 95.9%; Pred. No. 6e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 728 GAGTCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 776

RESULT 11
AAQ76106
ID AAQ76106 standard; DNA; 1860 BP.

XX AC AAQ76106;
XX DT 25-MAR-2003 (revised)
XX DT 20-JUL-1995 (first entry)
XX DE Cucumber mosaic virus RNA-3 chimera encoding TOMV CP.
XX KM Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
XX KM virus resistance; disease resistance; transgenic plant; cross protection;
XX KM hypersensitive response; crop improvement; tomato;
XX KM Lycopersicon esculentum; tobacco; Nicotiana tabacum; coat protein; CP;
XX KM TOMV; CMV; SG.
XX OS Cucumber mosaic virus.
XX
XX FH Key Location/Qualifiers
XX FT CDS 123..600
XX FT /*tag= a
XX FT /product= "TOMV coat protein"
XX FT 895..1550
XX FT /*tag= b
XX FT /product= "CMV coat protein"
XX
XX PN WO9429464-A1.
XX PD 22-DEC-1994.
XX
XX PF 03-JUN-1994; 94WO-EP001817.
XX PR 04-JUN-1993; 93GB-00011593.
XX
XX PA (SANO) SANDOZ LTD.
XX PA (SANO) SANDOZ PATENT GMBH.
XX PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
XX PI De Haan PT;
XX
XX DR WPI; 1995-036490/05.
XX DR P-PSDB; AAR67752, AAR67753.
XX
XX PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
XX PT encodes RNA that interacts with viral RNA polymerase to generate an
XX PT eliciting agent.
XX
XX PS Claim 3; Page 27-28; 50pp; English.
XX
XX CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76106) codes for the
XX CC coat protein (CP) of tomato mosaic virus (AAR67752) as well as its own CP
XX CC (AAR67753). The construct elicits minus-sense RNA that interacts with the
XX CC RNA-dependent RNA-polymerase of an invading virus, thus conferring virus-
XX CC resistance on a host plant, e.g. tobacco, tomato. (updated on 25-MAR-2003
XX CC to correct PN field.)
XX
XX SQ Sequence 1860 BP; 448 A; 429 C; 431 G; 552 T; 0 U; 0 Other;

Query Match 86.4%; Score 45.8; DB 2; Length 1860;
Best Local Similarity 95.9%; Pred. No. 6.1e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 892 GAGTCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 940

RESULT 12
AAQ76108
ID AAQ76108 standard; DNA; 2173 BP.

XX AC AAQ76108;
XX DT 25-MAR-2003 (revised)
XX DT 20-JUL-1995 (first entry)
XX DE Cucumber mosaic virus RNA-3 chimera encoding TOMV P30.
XX
XX KM Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
XX KM virus resistance; disease resistance; transgenic plant; cross protection;
XX KM hypersensitive response; crop improvement; tomato;
XX KM Lycopersicon esculentum; tobacco; Nicotiana tabacum; P30; elicitor; TOMV;
XX KM CMV; SG.
XX OS Cucumber mosaic virus.
XX
XX FH Key Location/Qualifiers
XX FT CDS 123..914
XX FT /*tag= a
XX FT /product= "TOMV P30 elicitor"
XX
XX PN WO9429464-A1.
XX PD 22-DEC-1994.
XX
XX PF 03-JUN-1994; 94WO-EP001817.
XX PR 04-JUN-1993; 93GB-00011593.
XX
XX PA (SANO) SANDOZ LTD.
XX PA (SANO) SANDOZ PATENT GMBH.
XX PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
XX PI De Haan PT;
XX
XX DR WPI; 1995-036490/05.
XX DR P-PSDB; AAR67755.
XX
XX PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
XX PT encodes RNA that interacts with viral RNA polymerase to generate an
XX PT eliciting agent.
XX
XX PS Claim 5; Page 34-35; 50pp; English.
XX
XX CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76108) has the coat
XX CC protein gene replaced by a gene encoding an elicitor, TOMV P30, having
XX CC the sequence given in AAR67755. The construct elicits a minus-sense RNA
XX CC that interacts with the RNA-dependent RNA-polymerase of an invading
XX CC virus, thus conferring virus-resistance on a host plant, e.g. tobacco,
XX CC tomato. (updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 2173 BP; 561 A; 438 C; 532 G; 642 T; 0 U; 0 Other;

Query Match 86.4%; Score 45.8; DB 2; Length 2173;
Best Local Similarity 95.9%; Pred. No. 6.3e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1205 GAGTCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 1253

RESULT 13
AAT34664

ID	AAT34664 standard; DNA; 772 BP.			
XX	AAT34664;			
AC	16-OCT-2003 (revised)			
XX	02-DEC-1996 (first entry)			
DT	Coat protein of the V27 strain of cucumber mosaic virus.			
XX				
XX	Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;			
KW	resistance; 88.			
XX				
OS	Cucumber mosaic virus; strain V27.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	3..659		
FT	/*tag= a			
XX				
PN	WO9621018-A1.			
XX				
PD	11-JUL-1996.			
XX				
PF	07-JUN-1995;	95WO-US007234.		
XX				
PR	30-DEC-1994;	94US-00367789.		
XX				
PA	(ASGR-) ASGROW SEED CO.			
XX				
PI	Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KU;			
XX				
DR	WPI; 1996-333993/33.			
DR	P-PSDB; AAR98893.			
XX				
PT	New isolated cucumber mosaic virus coat protein DNA - used to produce			
PT	plants, partic. of the family Cucurbitaceae or Solanaceae, which are			
PT	resistant to infection.			
XX				
PS	Claim 2; Fig 1; 80pp; English.			
XX				
CC	Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber			
CC	mosaic virus (CMV) were isolated. The CMV CP genes were isolated from			
CC	infected plant tissue by PCR amplification of cDNA using primers based on			
CC	known CP sequences. The genes may be used for producing plants such as			
CC	quash, cucumber, peppers and tomatoes which are resistant to CMV			
CC	infection. (Updated on 16-OCT-2003 to standardise OS field)			
XX				
XX				
SO	Sequence 772 BP; 177 A; 202 C; 182 G; 211 T; 0 U; 0 Other;			
Query Match 83.8%; Score 44.4; DB 2; Length 772;				
Best Local Similarity 97.8%; Pred. No. 1.8e-07;				
Matches 45; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	4 CCATGGACAAATCTGAATCAACAGTGTGCTGTAACCGTCGACG 49			
Ddb	1 CCATGGACAAATCTGAATCAACAGTGTGCTGTAACCGTCGACG 46			
RESULT 14				
ID	AAT17259			
XX	AAT17259 standard; DNA; 772 BP.			
XX	AAT17259;			
AC	16-OCT-2003 (revised)			
XX	02-DEC-1996 (first entry)			
DT	Coat protein of the A35 strain of cucumber mosaic virus.			
XX				
XX	Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;			
KW	resistance; 88.			
XX				
OS	Cucumber mosaic virus; strain A35.			
XX				

Key	Location/Qualifiers
FT CDS	3..659
FT	/*tag= a
XX	
XX	WO9621018-A1.
XX	
XX	11-JUL-1996.
XX	
XX	07-JUN-1995; 95WO-US007234.
PF	
XX	
PR	30-DEC-1994; 94US-00367789.
XX	
PA	(ASGR-) ASGROW SEED CO.
XX	
PI	Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX	
XX	WPI; 1996-333993/33.
DR	P-PSDB; AAR93803.
XX	
PT	New isolated cucumber mosaic virus coat protein DNA - used to produce
PT	plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT	resistant to infection.
XX	
PS	Disclosure; Fig 8; 80pp; English.
XX	
CC	Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC	mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC	infected plant tissue by PCR amplification of cDNA using primers based on
CC	known CP sequences. The genes may be used for producing plants such as
CC	quash, cucumber, peppers and tomatoes which are resistant to CMV
CC	infection. (Updated on 16-OCT-2003 to standardise OS field)
XX	
SQ	Sequence 772 BP; 175 A; 201 C; 185 G; 211 T; 0 U; 0 Other;
Query Match	83.8%; Score 44.4; DB 2; Length 772;
Best Local Similarity	97.8%; Pred. No. 1.8e-07;
Matches 45; Conservative	0; Mismatches 1; Indels 0; Gaps 0
QY	4 CCATGGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTGACG 49
Db	1 CCATGGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTGCGG 46
RESULT 15	
ID	AAN90249 standard; DNA; 1423 BP.
XX	
AC	AAN90249;
XX	
DT	24-OCT-2003 (revised)
DT	25-MAR-2003 (revised)
DT	01-NOV-1989 (first entry)
XX	
DE	Cucumber mosaic virus C coat protein gene.
XX	
KW	Cucumber mosaic virus C strain; virus-resistant plants; cucurbitacea;
KW	solanacea.
XX	
OS	Cucumber mosaic virus; C strain.
XX	
PN	WO8905858-A.
XX	
PD	29-JUN-1989.
XX	
PF	08-DEC-1988; 88WO-US004321.
XX	
PR	21-DEC-1987; 87US-00135591.
XX	
PA	(UPJO) UPJOHN CO.
XX	
PI	Quemada H, Slightom JL;
XX	
DR	WPI; 1989-206617/28.

XX Coat protein gene from C strain of cucumber mosaic virus - used to
PT prepare plant transformation vectors and virus-resistant plants.
PT
XX
PS Claim 1; Page 15; 19pp; English.
XX
CC Coat protein gene from cucumber mosaic virus C strain is inserted into a
CC transformation vector also comprising the 35S promoter of cauliflower
CC mosaic virus, and the polyadenylation signal of either the CaMV 35S gene
CC or the phaseolus vulgaris seed storage gene. This is used to transform
CC plants of cucurbitacea and solanacea to produce virus-resistant plants.
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 1423 BP; 385 A; 337 C; 320 G; 381 T; 0 U; 0 Other;

Query Match 83.4%; Score 44.2; DB 1; Length 1423;
Best Local Similarity 93.9%; Pred. No. 2.5e-07;
Matches 46; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
||| |||||
Db 370 GAGTCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCATCGACG 418

Search completed: December 5, 2004, 06:13:16
Job time : 227 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 03:35:58 ; Search time 1476 Seconds
(without alignments)
1308.473 Million cell updates/sec

Title: US-09-857-841-3

Perfect score: 53
Sequence: 1 gatccatggacaatctgaa.....gtcgtaacccgtcgacgagct 53

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hlc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45.8	86.4	127	4	BM067231 KS08001E1
2	25.8	48.7	200	7	H07817 H07817 kht1009 BNL
3	24.4	46.0	571	1	AV589910 AV589910
4	24.2	45.7	711	1	CR153168 Forward s
5	24.2	45.7	807	8	CC140418
6	24.2	45.7	1061	5	BX376013 BX376013
7	24	45.3	350	9	CG880078
8	24	45.3	465	6	CD122050
9	24	45.3	497	6	CD121836 ME1-0070P
10	24	45.3	751	8	AZ339011 1M0070L18
11	23.8	44.9	417	4	BJ232993 BJ232993
12	23.8	44.9	573	4	BI360440
13	23.8	44.9	609	5	BX922152 BX922152
14	23.6	44.5	631	7	CN698549 E0409C12-
15	23.6	44.5	666	9	CL708124 OR_BBa002
16	23.6	44.5	703	7	CO703958 DG32-270K
17	23.6	44.5	772	9	CL733950 OR_BBa006
18	23.6	44.5	952	9	CG882815 ZMMBB049
19	23.6	44.5	953	9	CC815885 ZMMBB052
20	23.4	44.2	372	5	BM967398 EST30 Tom
21	23.4	44.2	409	2	BE433897 EST404975
22	23.4	44.2	447	2	BE435780 EST406858
23	23.4	44.2	448	2	BE431932 EST398461
24	23.4	44.2	471	8	AQ666369 HS_5367_B

C	25	23.4	44.2	494	2	AW933614	AW933614	EST359457
C	26	23.4	44.2	507	2	BE434784	BE434784	EST405862
C	27	23.4	44.2	509	2	BE433535	BE433535	EST400064
C	28	23.4	44.2	525	2	BE461053	BE461053	EST412472
C	29	23.4	44.2	539	2	BE436288	BE436288	EST407366
C	30	23.4	44.2	544	2	BE460657	BE460657	EST412076
C	31	23.4	44.2	567	2	AW220906	AW220906	EST297375
C	32	23.4	44.2	569	2	BF112783	BF112783	EST440373
C	33	23.4	44.2	570	2	BE462001	BE462001	EST413339
C	34	23.4	44.2	571	2	BE460690	BE460690	EST412109
C	35	23.4	44.2	596	2	BE436895	BE436895	EST408013
C	36	23.4	44.2	607	2	BE434904	BE434904	EST405982
C	37	23.4	44.2	612	2	BF051011	BF051011	EST436186
C	38	23.4	44.2	614	2	BF113438	BF113438	EST441028
C	39	23.4	44.2	617	2	AW221834	AW221834	EST298645
C	40	23.4	44.2	627	8	BH977843	BH977843	odel4c11.
C	41	23.4	44.2	629	2	AW221911	AW221911	EST298722
C	42	23.4	44.2	632	2	BE434157	BE434157	EST405235
C	43	23.4	44.2	642	2	BE435313	BE435313	EST406391
C	44	23.4	44.2	667	2	AW442094	AW442094	EST311490
C	45	23.4	44.2	674	2	AW934244	AW934244	EST360087

ALIGNMENTS

RESULT 1
BM067231/c
LOCUS KS08001E12 KS08 Capsicum annuum cDNA, mRNA sequence.
DEFINITION
ACCESSION BM067231
VERSION BM067231.1 GI:22787366
KEYWORDS
SOURCE
ORGANISM
EST.
Capsicum annuum
Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Capsicum.

REFERENCE
1 (bases 1 to 127)
Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S.,
Hur,C.-G. and Choi,D.
Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
annuum L.) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen
Unpublished (2001)
Contact: Doll Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doil@mail.kribb.re.kr
High quality sequence stop: 127.

TITLE

JOURNAL
COMMENT

FEATURES
source

/organism="Capsicum annuum"
/mol_type="mRNA"
/cultiivar="Hang Keun"
/db_xref="taxon:4072"
/tissue_type="anther"
/dev_stage="10 weeks after germination"
/clone_lib="KS08"
/note="Vector: pBluescript SK(-)"

ORIGIN

Query Match 86.4%; Score 45.8; DB 4; Length 127;
Best Local Similarity 95.9%; Pred. No. 3.4e-07;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 83 GAGTCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 35

RESULT 2
LOCUS H07817/c 200 bp mRNA linear EST 23-JUN-1995
DEFINITION kb1009 BNLI Brassica napus cDNA 3', mRNA sequence.
ACCESSION H07817
VERSION H07817.1 GI:872639
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 200)
Sohn,U., Lee,C.M., Cho,K.H., Jeon,Y.H., Hahn,T.R. and Nam,H.G.
CDNAs from Brassica napus (rape)
Unpublished (1995)
Other_ESTs: Arabidopsis dbEST T44633
Contact: Uik Sohn
Laboratory of Molecular Biology
Kyungpook National University
Dept. of Genetic Eng., Kyungpook National Univ., Taegu 702-701, Korea
Tel: 0539505382
Fax: 0539555327
Email: usohn@bh.kyungpook.ac.kr
EST is putatively homologous to Arabidopsis dbEST T44633
Seq primer: M13 forward
Location/Qualifiers
1..200
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Naehan"
/db_xref="taxon:3708"
/lab_host="NM522"
/clone_lib="BNLI"
/note="Vector: pT7T3D; Site 1: NotI; Site 2: EcoRI;
Poly(A)-mRNA was purified from the leaf of B.napus.
cDNA library was constructed from the mRNAs by
oligo(dT) priming and directionally cloned from the NotI
site in the vector pT7T3D (Pharmacia) to the EcoRI site."

ORIGIN
Query Match 48.7%; Score 25.8; DB 7; Length 200;
Best Local Similarity 67.9%; Pred. No. 28;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GATCCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACGACT 53
|||||
200 GATCACAGCTGCATCTGATCGAACCGTGTGTGTCGTCACTGACGATCT 148
|||||

RESULT 3
LOCUS AV589910 571 bp mRNA linear EST 27-NOV-2001
DEFINITION AV589910 Bos taurus brain fetus Bos taurus cDNA clone E1BR009C12
5', mRNA sequence.
ACCESSION AV589910
VERSION AV589910.1 GI:9700903
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 571)
Takesuga,A., Hirotsune,S., Itch,R., Jitohzono,A., Suzuki,H., Aso,H.
and Sugimoto,Y.
Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs
Nucleic Acids Res. 29 (22), E108 (2001)
JOURNAL MEDLINE 21570554
PUBMED 11713328

COMMENT
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cococ.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
1..571
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="E1BR009C12"
/issue_type="brain"
/dev_stage="fetus"
/lab_host="DH10B"
/clone_lib="Bos taurus brain fetus"
/note="Vector: pZl1; Site 1: SalI; Site 2: NotI; Poly A
was deleted from a NotI site"

ORIGIN
Query Match 46.0%; Score 24.4; DB 1; Length 571;
Best Local Similarity 73.8%; Pred. No. 1.2e+02;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 ATCCATGACAATCTGAATCAACCAAGTGTGCTGCTAACC 43
|||||
Db 264 ATCCATGACCAAGTGTACAAACAGAGCTGCAGTTAACG 305
|||||

RESULT 4
LOCUS CR153168 711 bp DNA linear GSS 06-JUL-2004
DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and
chromosome engineering clone MHPN77n06, genomic survey sequence.
ACCESSION CR153168
VERSION CR153168.1 GI:49932013
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 711)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
Location/Qualifiers
1..711
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN77n06"
/clone_lib="MHPN"

ORIGIN
Query Match 45.7%; Score 24.2; DB 9; Length 711;
Best Local Similarity 71.1%; Pred. No. 1.4e+02;
Matches 32; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 ATCCATGACAATCTGAATCAACCAAGTGTGCTGTAACCGTCG 46
|||||
Db 585 ATATATGCTCCATCTTAATAAACCAAGTGTGACCTAACAGTTG 629
|||||

RESULT 5
LOCUS CC140418 807 bp DNA linear GSS 16-APR-2003
DEFINITION CC140418
NDL.2417.SP6 Notre Dame Liverpool Aedes aegypti genomic clone

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
NDL.2417				genomic survey sequence.
CC140418				
CC140418.1	GI:30009473			
GSS.				
Aedes aegypti				(yellow fever mosquito)
Aedes aegypti				
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
1	(bases 1 to 807)			
Loftus, B., Shetty, J., Knudson, D. and Severson, D.				
BAC end sequencing of Aedes aegypti				
Unpublished (2003)				
Other_GSSs: NDL.2417.T7				
Contact: Brendan Loftus				
Department of Eukaryotic Genomics				
TIGR				
9712 Medical Center Drive, Rockville, MD 20850, USA				
Tel: 301-838-3543				
Fax: 301-838-0208				
Email: enta@tigr.org				
Library was provided by David Severson				
Seq primer: SP6				
Class: BAC ends.				
Location/Qualifiers				
1..807				
/organism="Aedes aegypti"				
/mol_type="genomic DNA"				
/strain="Liverpool"				
/db_xref="taxon:7159"				
/clone="NDL.2417"				
/clone_lib="Notre Dame Liverpool"				
/note="Vector: pECBAC1; Site_1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"				
ORIGIN				
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Best Local Similarity	71.1%;	Pred. No. 1.5e+02;		
Matches 32;	Conservative 0;	Mismatches 13;	Indels 0;	Gaps 0;
Db	599	AACCATGCTACATTTGAATGACCCCATCCTGTCGAGCCGCTG	643	
2	ATCCATGACAAATCTGAATCAACACAGTGTGTCGTAACCGTCG	46		
BX376013	Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens			
CDNA clone CS0DC021YM11 3-PRIME, mRNA sequence.				
ACCESSION	BX376013			
VERSION	BX376013.2	GI:46555591		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1	(bases 1 to 1061)			
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
Full-length cDNA libraries and normalization				
Unpublished (2001)				
On May 8, 2003 this sequence version replaced gi:30434740.				
COMMENT				
Contact: Genoscope				
Genoscope - Centre National de Sequencage				
BP 191 91006 EVRY cedex - France				
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr				
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster				

2789.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CS0DC021AG06NP1&c=2789.f>.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC021YM11"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 45.7%; Score 24.2; DB 5; Length 1061;
Best Local Similarity 61.7%; Pred. No. 1.5e+02;
Matches 29; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 GATCCATGACAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGA 47
||||| :|:| | | | | | | | | | | | | | | :|
Db 1009 GATCCTTGCCMMMTGAGAGATGATCCATTGCGGTCTCATCCAMGA 1055

RESULT 7
CG880078/c 350 bp DNA linear GSS 02-DEC-2003
LOCUS ZMMBB0504M22F ZMMBBb (HindIII) Zea mays genomic clone
DEFINITION ZMMBBb0504M22 5', genomic survey sequence.
ACCESSION CG880078
VERSION CG880078.1 GI:38610691
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 350)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PGR (2003c)
Unpublished (2003)
Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 85.
Location/Qualifiers
1..350
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
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/clone="ZMMBBb0504M22"
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/note="Vector: pCUGI; site_1: HindIII; site_2: HindIII"

ORIGIN
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Best Local Similarity 68.8%; Pred. No. 1.5e+02;
Matches 33; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 ATCCATGACAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 49
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[illegible]

SOURCE ORGANISM	Schistosoma mansoni Schistosoma mansoni
REFERENCE AUTHORS	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeida; Schistosomatoidae; Schistosomatidae; Schistosoma. 1 (bases 1 to 497) Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M., Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr., Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F., Ho, P.L., Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A., Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A., Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T., Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.
TITLE	Transcriptome analysis of the acelomate human parasite Schistosoma mansoni
JOURNAL MEDLINE PUBMED	Nat. Genet. 35 (2), 148-157 (2003) 22879926 12973350
COMMENT	Contact: Dr. Sergio Verjovski-Almeida Departamento de Bioquímica Instituto de Química - Universidade de Sao Paulo Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP, Brasil Tel: +55-11-3091-2173 Fax: +55-11-3091-2186 Email: verjo@iq.usp.br This sequence was derived from the PAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL http://bioinfo.iq.usp.br/schisto/ Plate: MEI-0070P-V169 row: 7 column: C.
FEATURES	location/Qualifiers 1..497 /organism="Schistosoma mansoni" /mol_type="mRNA" /db_xref="taxon:6183" /clone="MEI-0070P-V169-C07.B" /sex="mixed pool" /dev_stage="egg" /lab_host="Mus musculus" /clone_lib="MEI-0070" /note="Vector: pGEM T-easy"
ORIGIN	Query Match 45.3%; Score 24; DB 6; Length 497; Best Local Similarity 68.8%; Pred. No. 1.6e+02; Matches 33; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Cy Db	2 ATCCATGCACCAATCTGAATCAACCAGTGTGTCGTACCGTCGACG 49 267 ACCTATGTATAAATTGTCTGAAACCATTAATGACATACCGTCAACG 314
RESULT 10	AZ339011 751 bp DNA linear GSS 29-SEP-2000
LOCUS DEFINITION	IM0070L18F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0070L18 F, genomic survey sequence.
ACCESSION AZ339011	
VERSION	
KEYWORDS	AZ339011.1 GI:10412854
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE AUTHORS	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 751) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Query Match	44.9%;	Score 23.8;	DB 4;	Length 573;
Best Local Similarity	66.7%;	Pred. No. 2e+02;		
Matches 34;	Conservative 0;	Mismatches 17;	Indels 0;	Gaps 0;
Qy	3	TCCATGGACAAATCTGAATCAACCAAGTGTGCTGCTAACCGCTGCAGAGCT	53	
Db	52	TCCATTGAGAAAAGAGAGCAGCCAGTGTGCTGAGACAGTAGAAGAGGT	102	
RESULT 13				
LOCUS	BX922152	609 bp	mRNA	linear
DEFINITION	BX922152	Sus Scrofa library (scan)	Sus scrofa	CDNA clone
ACCESSION	BX922152			
VERSION	BX922152.1	GI:41139000		
KEYWORDS	EST.			
SOURCE	Sus scrofa (pig)			
ORGANISM	Sus scrofa			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
TITLE	1 (bases 1 to 609)			
JOURNAL	Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,			
COMMENT	Soares, M., Bonaldo, F. and Hathey, F.			
	A Pig Normalised Multi-Tissue CDNA Library			
	Unpublished (2003)			
	Contact: Tosser-Klopp G			

Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Clone distribution: AGENAE Resource centre, Francois PUMI,
Francois.Pumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du
genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,
FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0022 row: e column: 22.

FEATURES	Location/Qualifiers
source	1. .609

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/note="tissues: adipose tissue, brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo uretral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"

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Query Match	44.9%;	Score 23.8;	DB 5;	length 609;
Best Local Similarity	66.7%;	Pred. No. 2e+02;		
Matches 34;	Conservative 0;	Mismatches 17;	Indels 0;	Gaps 0;

QY 3 TCCATGGACAAATCTGAATCAACCAGTGTGTCGTAACCGTCGACGAGCT 53
 ||||| ||||| ||||| ||||| |||||
Db 74 TTCATTCAGAAAAGAAGACGACCGAGTGCTGCTGAGACAGTAGAAGAGGT 124

RESULT	14
CN698549	
LOCUS	CN698549
DEFINITION	E0409C12-5 NIA Mouse E11.5 whole embryo cDNA library (Long) Mus
	631 bp mRNA linear EST 18-MAY-2004

ACCESSION	musculus cDNA clone NIA.E0409C12 IMAGE:30869411 5', mRNA sequence
VERSION	CN698549
KEYWORDS	CN698549.1 GI:47467298
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 631) Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y., vanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C., Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L., Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S., Nagaraja,R., Boheler,K.R., Taub,D., Hodges,R.J., Longo,D.L., Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A., Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A., D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
TITLE	Transcriptome analysis of mouse stem cells and early embryos
JOURNAL	PLoS Biol. 1 (3), 410-419 (2003)
COMMENT	Contact: Dawood B. Dudekula

National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun-grc.nia.nih.gov
Plate: E0409 row: C column: 12
Seq primer: M13 Reverse
High quality sequence stop: 631
POLYA=No.

FEATURES	Location/Qualifiers
source	1. .631

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/tissue_type="whole embryo including extraembryonic
tissues at 11.5-days postcoitum"
/dev_stage="E11.5"
/lab_host="DH10B"
/clone_lib="NIA Mouse E11.5 whole embryo cDNA library
(long)"
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
Site_2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11541199]). Total
cDNAs were extracted from a pool of 3 embryos at 11.5-days
postcoitum. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer [Invitrogen:
5'-pGACTACTTCTAGATCGCGAGCGCCGCCCTTTT-TTTT-3'] from
2ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker lL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 3.3kb. The library was
constructed by Yulan Piao."

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Query Match	44.5%;	Score 23.6;	DB 7;	length 631;
Best Local Similarity	69.6%;	Pred. No. 2.4e+02;		
Matches 32;	Conservative	0;	Mismatches 14;	Indels 0;
				Gaps 0;

7 TGGACAAATCTGATTCACCAAGTGTGTCGTAACCGTCGAGAGC 52

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 08:16:57 ; Search time 2543 Seconds
(without alignments)
260.344 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSAGRNR 14

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 segs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
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10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
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2	69	100.0	130	6	AR031575 Sequence
3	69	100.0	130	6	AR065687 Sequence
4	69	100.0	130	6	AR097446 Sequence

5	69	100.0	130	6	I49964	I49964 Sequence 14
6	69	100.0	131	6	AR031572	AR031572 Sequence
7	69	100.0	131	6	AR065684	AR065684 Sequence
8	69	100.0	131	6	AR097443	AR097443 Sequence
9	69	100.0	131	6	I49961	I49961 Sequence 11
10	69	100.0	152	6	AR031570	AR031570 Sequence
11	69	100.0	152	6	AR031571	AR031571 Sequence
12	69	100.0	152	6	AR065682	AR065682 Sequence
13	69	100.0	152	6	AR065683	AR065683 Sequence
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15	69	100.0	152	6	AR097442	AR097442 Sequence
16	69	100.0	152	6	I49959	I49959 Sequence 9
17	69	100.0	152	6	I49960	I49960 Sequence 10
18	69	100.0	154	6	AR031573	AR031573 Sequence
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26	69	100.0	654	6	E01760	E01760 DNA encodin
27	69	100.0	654	14	AF444252	AF444252 Banana mo
28	69	100.0	657	14	AB070622	AB070622 Cucumbe
29	69	100.0	657	14	AB109909	AB109909 Cucumbe
30	69	100.0	657	14	AF198622	AF198622 Cucumbe
31	69	100.0	657	14	AF281864	AF281864 Cucumbe
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33	69	100.0	657	14	AF350450	AF350450 Cucumbe
34	69	100.0	657	14	AF368192	AF368192 Cucumbe
35	69	100.0	657	14	AF523339	AF523339 Cucumbe
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44	69	100.0	657	14	AF523348	AF523348 Cucumbe
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ALIGNMENTS

RESULT 1
BD261798
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
BD261798 53 bp DNA linear PAT 17-JUL-2003
Enhancement in protein production by higher plants using ubiquitin
or cucumber mosaic virus coating protein peptide.
BD261798
BD261798.1 GI:33071566
JP 2002532098-A/2.
Cucumber mosaic virus (cucumber mosaic cucumovirus)
Cucumber mosaic virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
Cucumovirus.
1 (bases 1 to 53)
Fang,R.X., Wu,J.L. and Chen,X.Y.
Enhancement in protein production by higher plants using ubiquitin
or cucumber mosaic virus coating protein peptide
Patent: JP 2002532098-A 2 02-OCT-2002;
INSTITUTE OF MOLECULAR AGROBIOLOGY
OS Cucumber mosaic virus
PN JP 2002532098-A/2
PD 02-OCT-2002
PF 11-DEC-1998 JP 2000588378
PI RONG XIANG FANG,JUNG LIN WU,XIAO YING CHEN
PC C12N15/09,A01H5/00,C07K14/415,C07K19/00,C12N5/10,C12N15/00, PC
C12N5/00
CC Enhancement in protein production by higher plants using
ubiquitin or
cucumber mosaic virus coating protein peptide FH Key

Location/Qualifiers
(6)..(47).
FT CDS Location/Qualifiers
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/db_xref="taxon:12305"
ORIGIN
Alignment Scores:
Pred. No.: 0.000526 Length: 53
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-857-841-4 (1-14) x BD261798 (1-53)
QY 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 6 ATGGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGA 47
RESULT 2
AR031575 130 bp DNA linear PAT 29-SEP-1999
LOCUS AR031575
DEFINITION Sequence 14 from patent US 5866384.
ACCESSION AR031575
VERSION AR031575.1 GI:5945864
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
Unclassified.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 14 02-FEB-1999;
FEATURES
source 1..130
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 0.00137 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-857-841-4 (1-14) x AR031575 (1-130)
QY 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 53 ATGGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGA 94
RESULT 3
AR065687 130 bp DNA linear PAT 29-SEP-1999
LOCUS AR065687
DEFINITION Sequence 14 from patent US 5849548.
ACCESSION AR065687
VERSION AR065687.1 GI:5995903
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
Unclassified.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 14 15-DEC-1998;
FEATURES
source 1..130
Location/Qualifiers

/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 0.00137 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-857-841-4 (1-14) x AR065687 (1-130)
QY 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 53 ATGGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGA 94
RESULT 4
AR097446 130 bp DNA linear PAT 14-FEB-2001
LOCUS AR097446
DEFINITION Sequence 14 from patent US 6071730.
ACCESSION AR097446
VERSION AR097446.1 GI:12806176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
Unclassified.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 14 06-JUN-2000;
FEATURES
source 1..130
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 0.00137 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-857-841-4 (1-14) x AR097446 (1-130)
QY 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 53 ATGGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGA 94
RESULT 5
I49964 130 bp DNA linear PAT 07-OCT-1997
LOCUS I49964
DEFINITION Sequence 14 from patent US 5641673.
ACCESSION I49964
VERSION I49964.1 GI:2472184
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
Unclassified.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5641673-A 14 24-JUN-1997;
FEATURES
source 1..130
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:

Pred. No.: 0.00137 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x I49964 (1-130)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
53 ATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGA 94

RESULT 6

AR031572 AR031572 131 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 11 from patent US 5866384.
ACCESSION AR031572
VERSION AR031572.1 GI:5945861
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 11 02-FEB-1999;
FEATURES
source
1. .131
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 0.00138 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR031572 (1-131)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
54 ATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGA 95

RESULT 7

AR065684 AR065684 131 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 11 from patent US 5849548.
ACCESSION AR065684
VERSION AR065684.1 GI:5995900
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 11 15-DEC-1998;
FEATURES
source
1. .131
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 0.00138 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR065684 (1-131)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
54 ATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGA 95

RESULT 8

AR097443 AR097443 131 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 11 from patent US 6071730.
ACCESSION AR097443
VERSION AR097443.1 GI:12806173
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 11 06-JUN-2000;
FEATURES
source
1. .131
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 0.00138 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR097443 (1-131)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
54 ATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGA 95

RESULT 9

I49961 I49961 131 bp DNA linear PAT 07-OCT-1997
LOCUS
DEFINITION Sequence 11 from patent US 5641673.
ACCESSION I49961
VERSION I49961.1 GI:2472181
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5641673-A 11 24-JUN-1997;
FEATURES
source
1. .131
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 0.00138 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x I49961 (1-131)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14

Db 54 ATGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGA 95

RESULT 10

LOCUS AR031570 152 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 9 from patent US 5866384.
ACCESSION AR031570
VERSION AR031570.1 GI:5945859
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 9 02-FEB-1999;
FEATURES Location/Qualifiers

source 1..152

/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 0.00162 Length: 152
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR031570 (1-152)

Qy 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 75 ATGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGA 116

RESULT 11

LOCUS AR031571 152 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 10 from patent US 5866384.
ACCESSION AR031571
VERSION AR031571.1 GI:5945860
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 10 02-FEB-1999;
FEATURES Location/Qualifiers

source 1..152

/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 0.00162 Length: 152
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR031571 (1-152)

Qy 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 75 ATGATTAATCTGAATCAACCAAGTGTGTCGTAACCGTCGA 116

RESULT 12

AR065682

LOCUS AR065682 152 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 9 from patent US 5849548.
ACCESSION AR065682
VERSION AR065682.1 GI:5995898
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 9 15-DEC-1998;
FEATURES Location/Qualifiers

source 1..152

/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 0.00162 Length: 152
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR065682 (1-152)

Qy 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 75 ATGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGA 116

RESULT 13

LOCUS AR065683 152 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 10 from patent US 5849548.
ACCESSION AR065683
VERSION AR065683.1 GI:5995899
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 10 15-DEC-1998;
FEATURES Location/Qualifiers

source 1..152

/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 0.00162 Length: 152
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR065683 (1-152)

Qy 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 75 ATGATTAATCTGAATCAACCAAGTGTGTCGTAACCGTCGA 116

RESULT 14

LOCUS AR097441 152 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 9 from patent US 6071730.
ACCESSION AR097441
VERSION AR097441.1 GI:12806171
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 9 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..152
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 0.00162 Length: 152
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR097441 (1-152)

OY 1 MetAplysSerGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
DB 75 ATGACAAATCTGAATCAACCAGTGTGTGTAACCGTCA 116
RESULT 15
AR097442 152 bp DNA linear PAT 14-FEB-2001
LOCUS AR097442
DEFINITION Sequence 10 from patent US 6071730.
ACCESSION AR097442
VERSION AR097442.1 GI:12806172
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 10 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..152
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 0.00162 Length: 152
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR097442 (1-152)

OY 1 MetAplysSerGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
DB 75 ATGATTAATCTGAATCAACCAGTGTGTGTAACCGTCA 116

Search completed: December 5, 2004, 09:07:02
Job time : 2544 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 08:15:22 ; Search time 326 Seconds
(without alignments)
225.435 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSGRNRR 14

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	69	100.0	53	3	AAA30858
2	69	100.0	771	2	AAT34666
3	69	100.0	772	2	AAT34664
4	69	100.0	772	2	AAT17259
5	69	100.0	773	2	AAT34665
6	69	100.0	976	2	AAQ10461

7	69	100.0	1007	2	AAQ10462	Aaql0462 Capsid pr
8	69	100.0	1007	2	AAQ67395	Aaql0462 Cauliflow
9	69	100.0	1066	2	AAT99545	Aaql0462 Cucumbe
10	69	100.0	1067	2	AAZ07505	Aaql0462 Cucumbe
11	69	100.0	1379	1	AAAN8111	Aaql0462 Sequence
12	69	100.0	1696	2	AAQ76107	Aaql0462 Cucumbe
13	69	100.0	1860	2	AAQ76106	Aaql0462 Cucumbe
14	69	100.0	2173	2	AAQ76108	Aaql0462 Cucumbe
15	64	92.8	657	2	AAQ03641	Aaql0462 Cucumbe
16	64	92.8	1423	1	AAAN90249	Aaql0462 Cucumbe
17	64	92.8	1426	2	AAT72272	Aaql0462 Cucumbe
18	61	88.4	894	3	ABL58209	Abi58209 Agrobacte
19	45	65.2	399	10	ABZ37724	Abz37724 N. gonorr
20	45	65.2	399	10	ABZ41931	Abz41931 N. gonorr
21	44	63.8	1317	12	ADO61972	Ado61972 Transcrip
22	44	63.8	1603	8	ACA38515	Ac38515 Prokaryot
23	44	63.8	2208	11	ABD15071	Abd15071 Pseudomon
24	44	63.8	2361	11	ABD15266	Abd15266 Pseudomon
25	44	63.8	2625	8	ACA40580	Ac40580 Prokaryot
26	44	63.8	2862	11	ABD14864	Abd14864 Pseudomon
27	44	63.8	110000	4	AAI99682_22	Continuation (23 o
28	44	63.8	110000	4	AAI99682_23	Continuation (24 o
29	44	63.8	110000	4	AAI99683_23	Continuation (24 o
30	43	62.3	401	5	AAF66292	Aaf66292 Novel hum
31	43	62.3	2000	8	ADA72454	Ada72454 Rice gene
32	43	62.3	2000	8	ADA72516	Ada72516 Rice gene
33	43	62.3	125439	6	ABQ88177	Abq88177 Human ost
34	358	60.9	358	12	ADP59136	Adp59136 Maize car
35	42	60.9	656	3	AAC50398	Aac50398 Arabidops
36	42	60.9	657	2	AAQ41742	Aaq41742 Cucumbe
37	42	60.9	657	2	AAQ80683	Aaq80683 CMV-SA co
38	42	60.9	657	3	AAC34260	Aac34260 Arabidops
39	42	60.9	700	4	AAH92121	Aah92121 Human inf
40	42	60.9	979	11	ABD17977	Abd17977 Human ade
41	42	60.9	980	10	ABZ97241	Abz97241 Human ade
42	42	60.9	981	2	AAQ48414	Aaq48414 Human Al
43	42	60.9	981	2	AAT07648	Aat07648 Human ade
44	42	60.9	981	2	AAT29929	Aat29929 Human ven
45	42	60.9	981	2	AAT00644	Aat00644 Human Al

ALIGNMENTS

RESULT 1	AAA30858	standard; DNA; 53 BP.
ID	AAA30858	
XX	AAA30858;	
AC	19-SEP-2000	(first entry)
XX		
DT	Ubiquitin monomer C-terminal fragment coding sequence.	
XX		
DB	Ubiquitin monomer; protein production; plant cell; ubiquitin promoter;	
XX		
KW	ds.	
XX		
OS	Nicotiana tabacum.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	6..47
FT		/*tag= a
FT		/product= "Ubiquitin_monomer_fragment"
FT		/partial
XX		
PN	WO200036129-A1.	
XX		
PD	22-JUN-2000.	
XX		
PF	11-DEC-1998;	98WO-SG000103.
XX		
PR	11-DEC-1998;	98WO-SG000103.
XX		
PA	(MOLE-) INST MOLECULAR AGROBIOLOGY.	

XX PI Fang R, Wu J, Chen X;
XX DR WPI; 2000-431604/37.
XX DR P-PSDB; AAY90255.
XX PT Production of desired protein in plants or plant cells by linking a
PT ubiquitin monomer coding sequence upstream of the gene encoding the
PT desired protein.
XX PS Claim 8; Page 18; 42pp; English.
XX CC This sequence encodes the C-terminal fragment of a ubiquitin monomer. The
CC invention relates to a method for enhancing production of a desired
CC protein in a plant or plant cell by inserting a nucleic acid (NA)
CC encoding a ubiquitin monomer upstream of a NA encoding the desired
CC protein, where the fusion construct encodes a fusion protein and
CC expression is not controlled by the ubiquitin promoter. The invention
CC also relates to a NA acid vector a NA vector able to transform a plant
CC cell, that comprises NA encoding a fusion protein having a ubiquitin
CC monomer linked to a protein of interest and further, where expression of
CC the fusion construct is not under control of a ubiquitin promoter. The
CC construct allows enhanced production of the desired protein in plants or
CC plant cells
XX SQ Sequence 53 BP; 15 A; 14 C; 13 G; 11 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000262 Length: 53
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-857-841-4 (1-14) x AAA30858 (1-53)

QY 1 MetAspIySSerGIuSerThrSerAlaGlyArgAsnArgArg 14
Db 6 ATGGACCAATCTGATCAACCACTGCTGCTGTAACCGTCGA 47

RESULT 2
AAT34666
ID AAT34666 standard; DNA; 771 BP.
XX AC AAT34666;
XX OS 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX DE Coat protein of the V34 strain of cucumber mosaic virus.
XX KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance; ss.
XX OS Cucumber mosaic virus; strain V34.
XX FH Key Location/Qualifiers
FH CDS 3..659
FT /*tag= a
XX PN WO9621018-A1.
XX PD 11-JUL-1996.
XX PF 07-JUN-1995; 95WO-US007234.
XX PR 30-DEC-1994; 94US-00367789.
XX PA (ASGR-) ASGROW SEED CO.
XX PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX

DR WPI; 1996-333993/33.
DR P-PSDB; AAR98895.
XX PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX PS Claim 24; Fig 3; 80pp; English.

XX CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 771 BP; 176 A; 199 C; 183 G; 213 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00572 Length: 771
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAT34666 (1-771)

QY 1 MetAspIySSerGIuSerThrSerAlaGlyArgAsnArgArg 14
Db 3 ATGGACCAATCTGATCAACCACTGCTGCTGTAACCGTCGA 44

RESULT 3
AAT34664
ID AAT34664 standard; DNA; 772 BP.
XX AC AAT34664;
XX OS 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX DE Coat protein of the V27 strain of cucumber mosaic virus.
XX KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance; ss.
XX OS Cucumber mosaic virus; strain V27.
XX FH Key Location/Qualifiers
FH CDS 3..659
FT /*tag= a
XX PN WO9621018-A1.
XX PD 11-JUL-1996.
XX PF 07-JUN-1995; 95WO-US007234.
XX PR 30-DEC-1994; 94US-00367789.
XX PA (ASGR-) ASGROW SEED CO.
XX PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX

XX WPI; 1996-333993/33.
XX DR P-PSDB; AAR98893.
XX PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX PS Claim 2; Fig 1; 80pp; English.

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 772 BP; 177 A; 202 C; 182 G; 211 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00573 Length: 772
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAT34664 (1-772)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
ID AAT17259
AC AAT17259; 3 ATGACAAATCTGAATCAACCACTGCTGCTGAACCGTCGG 44
XX
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the A35 strain of cucumber mosaic virus.
XX
KM Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance; ss.
XX
OS Cucumber mosaic virus; strain A35.
XX
FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a
XX
PN WO9621018-A1.
XX
PD 11-JUL-1996.
XX
XX 07-JUN-1995; 95WO-US007234.
PF 30-DEC-1994; 94US-00367789.
PR (ASGR-) ASGROW SEED CO.
XX
XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX PI
XX WPI; 1996-333993/33.
DR P-PSDB; AAR93803.
XX
XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
XX
PS Disclosure; Fig 8; 80pp; English.
XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 772 BP; 175 A; 201 C; 185 G; 211 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00573 Length: 772
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAT17259 (1-772)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
ID AAT34665 3 ATGACAAATCTGAATCAACCACTGCTGCTGAACCGTCGG 44
DB
XX
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the V33 strain of cucumber mosaic virus.
XX
KM Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance; ss.
XX
OS Cucumber mosaic virus; strain V33.
XX
FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a
XX
PN WO9621018-A1.
XX
PD 11-JUL-1996.
XX
XX 07-JUN-1995; 95WO-US007234.
PF 30-DEC-1994; 94US-00367789.
PR (ASGR-) ASGROW SEED CO.
XX
XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX PI
XX WPI; 1996-333993/33.
DR P-PSDB; AAR98894.
XX
XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
XX
PS Claim 13; Fig 2; 80pp; English.
XX
XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 773 BP; 175 A; 200 C; 185 G; 213 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00574 Length: 773
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAT34665 (1-773)

AAQ67395
ID AAQ67395 standard; DNA; 1007 BP.
XX
AC AAQ67395;
XX
DT 25-MAR-2003 (revised)
DT 12-APR-1995 (first entry)
XX
DB Cauliflower mosaic virus capsid protein coding sequence.
XX
KM Cauliflower mosaic virus; CMV; capsid protein; coat protein;
KM polyribozyme; inactivate; inactivation; resistance; crop protection; ss.
XX
OS Cauliflower mosaic virus.
XX
FH Key Location/Qualifiers
FT CDS 54..710
FT /*tag= a
FT /product= "Capsid protein."
XX
XX FR2701960-A1.
XX
XX PD 02-SEP-1994.
XX
XX PF 26-FEB-1993; 93FR-00002269.
XX
XX PR 26-FEB-1993; 93FR-00002269.
XX
XX PA (GENE-) GENE SHEARS PTY LTD.
XX
XX PI Lenee P, Perez P, Gruber V, Baudot G, Ollivo C;
XX
XX DR WPI; 1994-281767/35.
XX
XX DR P-PSDB; AAR57968.
XX
XX PT New polyribozyme contg. several catalytic regions in complementary
PT sequence - can inactivate gene for viral capsid protein, esp. for prepn.
PT of new virus resistant transgenic plants, also DNA sequence encoding it.
XX
XX PS Disclosure; Fig 2; 67pp; French.
XX
XX CC The RNA encoding the capsid protein of cauliflower mosaic virus can be
CC targeted by a nucleic acid sequence called a "polyribozyme". The
CC polyribozyme has endoribonuclease activity and is able to inactivate the
CC gene encoding the viral capsid protein. The polyribozyme comprises
CC several catalytic regions derived from ribozymes and confers complete
CC resistance to virus. See AAQ67391-94. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
XX SQ Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0.00778 Length: 1007
XX Score: 69.00 Matches: 14
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-857-841-4 (1-14) x AAQ67395 (1-1007)
XX
QY 1 MetAspIySserGluSerThrSeraIaGlyARgAsnARgArg 14
Db 54 ATGACAAATCTGAATCAACCAAGTGTGTGTGTAACCGTGA 95
XX
XX RESULT 9
XX ID AAT99545 standard; cDNA; 1066 BP.
XX
XX AC AAT99545;
XX
XX DT 25-MAR-2003 (revised)
XX DT 21-MAY-1998 (first entry)

XX
DE Cucumber mosaic virus RNA-3 cDNA fragment.
XX
XX Transgenic plant; virus resistance; disease resistance; RNA virus; CMV;
KM coat protein; antisense gene; ss.
XX
XX Cucumber mosaic virus.
XX
XX FH Key Location/Qualifiers
FT 3'UTR 1..299
FT /*tag= a
FT CDS 300..958
FT /*tag= b
FT /*product= "coat protein"
FT sig_peptide 956..1029
FT /*tag= c
FT /*note= "coat protein leader sequence"
FT promoter 1030..1066
FT /*tag= d
FT /*note= "F sequence of sub-genomic promoter"
XX
XX EP806481-A2.
XX
XX PD 12-NOV-1997.
XX
XX PF 07-MAY-1997; 97EP-00201379.
XX
XX PR 09-MAY-1996; 96IT-MI000927.
XX
XX PA (META-) METAPONTUM AGROBIOS SCRL.
XX
XX PI Cellini F, Grieco PD;
XX
XX DR WPI; 1997-538620/50.
XX
XX PT Preparing transgenic plants resistant to RNA virus infection - using
PT anti:sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
XX PS Claim 3; Page 10; 18pp; English.
XX
XX CC This cDNA clone of cucumber mosaic virus (CMV) RNA-3 includes domain F of
XX the subgenomic promoter of viral RNA, the coat protein gene, its leader
XX sequence, and the tRNA-like 3'-terminal region of RNA-3. It was prepared
XX by amplifying a fragment of CMV cDNA-3 from clone PCR-CMV:RNA3 by PCR
XX (see also AAT99548-49). The gene construct is introduced into a vector
XX containing a promoter active in plant cells in antisense orientation
XX relative to the promoter. A claimed recombinant vector comprises the
XX plant promoter, the antisense gene construct and a terminator which is
XX functional in the plant. In addition to CMV, viral RNA may also be used
XX from tobacco mosaic virus and potato virus. Claimed transgenic plants
XX have the antisense gene construct integrated into their genomes. They are
XX resistant to viral infection. In particular, they are resistant to CMV.
XX Within the antisense gene construct, the interfering activity of the
XX antisense F domain of the sub-genomic promoter, associated with the
XX antisense activity performed by the coat protein gene, allows production
XX of plants having 100% resistance to CMV. (Updated on 25-MAR-2003 to
XX correct PR field.)
XX
XX SQ Sequence 1066 BP; 299 A; 251 C; 273 G; 243 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0.00831 Length: 1066
XX Score: 69.00 Matches: 14
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-857-841-4 (1-14) x AAT99545 (1-1066)
XX
QY 1 MetAspIySserGluSerThrSeraIaGlyARgAsnARgArg 14
XX
XX |||||

Db 956 ATGGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 915
RESULT 10
AAZ07505/c
ID AAZ07505 standard; cDNA; 1067 BP.
XX
AC AAZ07505;
XX
DT 26-NOV-1999 (first entry)
XX
DE Cucumber mosaic virus (CMV) RNA-3 gene cDNA clone fragment.
XX
KM Transgenic plant; RNA virus; antisense construct; cucumber mosaic virus;
CMV; promoter; coat protein gene; infection; RNA-3; ss.
XX
OS Cucumber mosaic virus.
XX
PN USS959181-A.
XX
PD 28-SEP-1999.
XX
PF 09-MAY-1997; 97US-00854170.
XX
PR 09-MAY-1996; 96IT-MI000927.
XX
PA (META-) METAPONTUM AGROBIOS SCLL.
XX
PI Cellini F, Grieco PD;
XX
DR WPI; 1997-538620/50.
XX
PT Preparing transgenic plants resistant to RNA virus infection - using
PT anti:sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
PS Claim 2; Fig 1; 15pp; English.
XX
CC The invention relates to preparing transgenic plants resistant to RNA
CC virus induced infections that comprises integrating an antisense gene
CC construct into the plant genome. The construct comprises: (a) an F domain
CC of a subgenomic promoter of cucumber mosaic virus (CMV); (b) downstream
CC from the subgenomic promoter, a leader sequence of a coat protein gene of
CC CMV; (c) downstream from the leader sequence, a gene encoding a CMV coat
CC protein; and (d) downstream from the gene, a 3'-terminal region of a CMV
CC coat protein gene. The method is useful for producing plants which are
CC resistant to infection by RNA based viruses. The gene construct gives
CC higher levels of resistance compared to antisense constructs which are
CC capable of complementing with different domains of genomic RNA of CMV.
CC The present sequence represents the fragment of cDNA clone of RNA-3 of
CC CMV. This forms the antisense construct of the invention
XX
SQ Sequence 1067 BP; 297 A; 250 C; 276 G; 244 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00832 Length: 1067
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAZ07505 (1-1067)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
ID AAN81111
AC AAN81111
XX
XX AAN81111; standard; DNA; 1379 BP.

Db 956 ATGGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 915
RESULT 11
AAN81111
ID AAN81111 standard; DNA; 1379 BP.
XX
AC AAN81111;
XX

DT 25-MAR-2003 (revised)
DT 12-NOV-1990 (first entry)
XX
XX Sequence contg. CMV strain Y coat protein gene.
XX
KM Cucumber mosaic virus; plant viral resistance; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 418..1074
FT /*tag= a
FT /label= cucumber mosaic virus-Y coat protein.
XX
PN EP279433-A.
XX
PD 24-AUG-1988.
XX
PF 18-FEB-1988; 88EP-00102322.
XX
PR 20-FEB-1987; 87JP-00038288.
PR 25-FEB-1987; 87JP-00043443.
PR 18-FEB-1988; 88JP-00035809.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Furusawa I, Onda H, Komiya T;
XX
XX WPI; 1988-236708/34.
DR P-PSDB; AAP80509.
XX
XX
PT DNA coding for the coat protein of cucumber mosaic virus strain Y - used
PT for producing plants resistant to cucumber mosaic virus infection.
XX
XX
PS Disclosure; Page ?; 20pp; English.
XX
XX This DNA is produced on screening of a plasmid library and is used to
CC transform plant cells which subsequently produce the coat prot- ein of
CC cucumber mosaic virus (CMV) strain Y. This protein is not synthesised in
CC natural plant cells. The resistance to CMV infect- ion, provided by the
CC DNA, is shown in plant cells and redifferent- iated plant bodies. See
CC also AAN81110. (Updated on 25-MAR-2003 to correct PR field.) (Updated on
XX 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1379 BP; 306 A; 342 C; 333 G; 398 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0112 Length: 1379
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-857-841-4 (1-14) x AAN81111 (1-1379)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
ID AAN81111
AC AAN81111
XX
XX AAN81111; standard; DNA; 1696 BP.

Db 418 ATGGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 459
RESULT 12
AAQ76107
ID AAQ76107 standard; DNA; 1696 BP.
XX
AC AAQ76107;
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE Cucumber mosaic virus RNA-3 chimera encoding RNase TI.
XX
XX Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KM virus resistance; disease resistance; transgenic plant; cross protection;

KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; RNase T1;
KW cell inhibitory protein; TOMV; CMV; ss.
XX
OS Cucumber mosaic virus.
XX
FH Key Location/Qualifiers
FT CDS 123..437
FT /*tag= a
FT /product= "RNase T1"
XX
PN W09429464-A1.
XX
PD 22-DEC-1994.
XX
PF 03-JUN-1994; 94WO-EP001817.
XX
PR 04-JUN-1993; 93GB-00011593.
XX
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI De Haan PT;
XX
DR WPI; 1995-036490/05.
DR P-PSDB; AAR67754.
XX
PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.
XX
PS Claim 4; Page 31-32; 50pp; English.
XX
CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76107) has the coat
CC protein gene replaced by a gene encoding a cell inhibitory protein, RNase
CC T1, having the sequence given in AAR67754. The construct elicits a minus-
CC sense RNA that interacts with the RNA-dependent RNA-polymerase of an
CC invading virus, thus conferring virus-resistance on a host plant, e.g.
CC tobacco, tomato. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 1696 BP; 387 A; 413 C; 389 G; 507 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0142 Length: 1696
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ76107 (1-1696)
QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
DB 733 ATGGACAAATCTGAATCAACCACTGCTGTCGTAAACCGTCGA 774

RESULT 13
AAQ76106
ID AAQ76106 standard; DNA; 1860 BP.
XX
AC AAQ76106;
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE Cucumber mosaic virus RNA-3 chimera encoding TOMV CP.
XX
KW Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; coat protein; CP;
KW TOMV; CMV; ss.

XX
OS Cucumber mosaic virus.
XX
FH Key Location/Qualifiers
FT CDS 123..600
FT /*tag= a
FT /product= "TOMV coat protein"
FT 895..1550
FT /*tag= b
FT /product= "CMV coat protein"
XX
PN W09429464-A1.
XX
PD 22-DEC-1994.
XX
PF 03-JUN-1994; 94WO-EP001817.
XX
PR 04-JUN-1993; 93GB-00011593.
XX
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI De Haan PT;
XX
DR WPI; 1995-036490/05.
DR P-PSDB; AAR67752, AAR67753.
XX
PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.
XX
PS Claim 3; Page 27-28; 50pp; English.
XX
CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76106) codes for the
CC coat protein (CP) of tomato mosaic virus (AAR67752) as well as its own CP
CC (AAR67753). The construct elicits minus-sense RNA that interacts with the
CC RNA-dependent RNA-polymerase of an invading virus, thus conferring virus-
CC resistance on a host plant, e.g. tobacco, tomato. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 1860 BP; 448 A; 429 C; 431 G; 552 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0158 Length: 1860
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ76106 (1-1860)
QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
DB 897 ATGGACAAATCTGAATCAACCACTGCTGTCGTAAACCGTCGA 938

RESULT 14
AAQ76108
ID AAQ76108 standard; DNA; 2173 BP.
XX
AC AAQ76108;
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE Cucumber mosaic virus RNA-3 chimera encoding TOMV P30.
XX
KW Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; P30; elicitor; TOMV;
KW CMV; ss.

XX OS Cucumber mosaic virus.
XX XX
FH Key Location/Qualifiers
FT CDS 123..914
FT /*tag= a
FT /product= "Tomv P30 elicitor"
XX
XX PN WO9429464-A1.
XX PD 22-DEC-1994.
XX PF 03-JUN-1994; 94WO-EP001817.
XX PR 04-JUN-1993; 93GB-00011593.
XX
XX PA (SANO) SANDOZ LTD.
XX PA (SANO) SANDOZ PATENT GMBH.
XX PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX PI De Haan PT;
XX
XX WPI; 1995-036490/05.
XX DR P-PSDB; AAR67755.
XX
PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.
XX
XX PS Claim 5; Page 34-35; 50pp; English.
XX
CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76108) has the coat
CC protein gene replaced by a gene encoding an elicitor, Tomv P30, having
CC the sequence given in AAR67755. The construct elicits a minus-sense RNA
CC that interacts with the RNA-dependent RNA-polymerase of an invading
CC virus, thus conferring virus-resistance on a host plant, e.g. tobacco,
CC tomato. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 2173 BP; 561 A; 438 C; 532 G; 642 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0189 Length: 2173
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ76108 (1-2173)

QY 1 MetAspLysSerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 1210 ATGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGA 1251

RESULT 15
AAQ03641
ID AAQ03641 standard; DNA; 657 BP.
XX
XX AAQ03641;
XX
DT 24-OCT-2003 (revised)
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 07-AUG-1990 (first entry)
XX
DE Cucumber Mosaic Virus-C (CMV-C) coat protein gene.
XX
XX CMV-C; curcubitaceae; solanaceae; ds.
XX
OS Cucumber mosaic virus; strain C.
XX
XX PN WO9002185-A.
XX

PD 08-MAR-1990.
XX
XX PF 02-AUG-1989; 89WO-US003288.
XX
XX PR 19-AUG-1988; 88US-00234404.
XX
XX PA (UPJO) UPJOHN CO.
XX PA (CORR) CORNELL RES FOUND INC.
XX
XX PI Quemada H, Slightom JL, Gonsalves D, Kearney C;
XX
XX DR WPI; 1990-099409/13.
XX
XX PT Coat protein gene of cucumber mosaic virus strain WL - cloned to produce
XX PT transformed plants which are resistant to CMV viral infection.
XX
XX PS Disclosure; Page ?; 18pp; English.
XX
XX CC The sequence encodes the coat protein of CMV-C. (Updated on 25-MAR-2003
XX CC to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)
XX CC (Updated on 27-AUG-2003 to correct OS field.) (Updated on 24-OCT-2003 to
XX CC standardise OS field)
XX
XX SQ Sequence 657 BP; 157 A; 176 C; 151 G; 173 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0379 Length: 657
Score: 64.00 Matches: 13
Percent Similarity: 92.86% Conservative: 0
Best Local Similarity: 92.86% Mismatches: 1
Query Match: 92.75% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ03641 (1-657)

QY 1 MetAspLysSerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 1 ATGACAAATCTGAATCAACCAAGTGTGTCGTAACCATCGA 42

Search completed: December 5, 2004, 08:24:35
Job time : 329 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 08:17:23 ; Search time 2044 Seconds
(without alignments)
249.587 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSAGRNR 14

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09857841/runat_03122004_160551_18593/app_query.fasta_1.199
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09857841@CGN_1_1_3437@runat_03122004_160551_18593 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_htc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	69	100.0	127	4	BM067231 KS08001E1
C 2	49	71.0	416	2	BE023342 BE023342 sm70f09.y
C 3	49	71.0	443	6	CA800884 sat26b02.
C 4	49	71.0	456	4	BI468772 BI468772 ga103c10.
C 5	49	71.0	544	4	BI971551 GM830013B
C 6	48	69.6	617	8	AQ737846 HS_2167_A
C 7	48	69.6	956	9	CC978898 ZUAG628TH
C 8	47	68.1	594	7	CF568862 FAMU USDA
C 9	46	66.7	413	1	AL584972 AL584972

C 10	46	66.7	480	1	AL836204	AL836204
C 11	46	66.7	486	5	BX256743	BX256743
C 12	46	66.7	490	5	BX256742	BX256742
C 13	46	66.7	645	6	CD356033	CD356033
C 14	46	66.7	653	7	CF577172	CF577172
C 15	46	66.7	677	9	AG540710	AG540710
C 16	46	66.7	703	5	BU340711	BU340711
C 17	46	66.7	709	9	CE629751	CE629751
C 18	46	66.7	754	5	BU109941	BU109941
C 19	46	66.7	760	5	BU366212	BU366212
C 20	46	66.7	804	5	BU261839	BU261839
C 21	46	66.7	813	5	BU256140	BU256140
C 22	46	66.7	815	5	BU227211	BU227211
C 23	46	66.7	842	5	BU323014	BU323014
C 24	46	66.7	899	5	BU134521	BU134521
C 25	46	66.7	1829	4	BM542237	BM542237
C 26	45	65.2	363	8	AQ770244	AQ770244
C 27	45	65.2	399	2	AW752426	AW752426
C 28	45	65.2	429	9	CC860753	CC860753
C 29	45	65.2	504	1	AI930097	AI930097
C 30	45	65.2	565	6	CB241923	CB241923
C 31	45	65.2	675	7	CF881443	CF881443
C 32	45	65.2	690	9	CE056926	CE056926
C 33	45	65.2	744	6	CF250879	CF250879
C 34	45	65.2	754	5	BU271993	BU271993
C 35	45	65.2	791	8	CC401658	CC401658
C 36	45	65.2	827	9	CC692105	CC692105
C 37	45	65.2	1093	4	BG404055	BG404055
C 38	44	63.8	248	2	BF519533	BF519533
C 39	44	63.8	315	1	AV161127	AV161127
C 40	44	63.8	400	8	AZ049482	AZ049482
C 41	44	63.8	404	2	AW127447	AW127447
C 42	44	63.8	413	1	AJ502914	AJ502914
C 43	44	63.8	422	5	BQ164765	BQ164765
C 44	44	63.8	471	8	AQ863793	AQ863793
C 45	44	63.8	476	1	AL369661	AL369661

ALIGNMENTS

RESULT 1
LOCUS BM067231/C 127 bp mRNA linear EST 11-SEP-2002
DEFINITION KS0801E12 KS08 Capsicum annuum cDNA, mRNA sequence.
ACCESSION BM067231
VERSION BM067231.1 GI:22787366
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Capsicum annuum

REFERENCE 1 (bases 1 to 127)
AUTHORS Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G. and Choi, D.
TITLE Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen

JOURNAL COMMENT

Unpublished (2001)
Contact: Doil Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doil@mail.kribb.re.kr
High quality sequence stop: 127.

FEATURES

source 1..127
/organism="Capsicum annuum"
/mol_type="mRNA"
/cultiivar="Hang Keun"
/db_xref="taxon:4072"

ORIGIN /cissue type="anther"
/dev_stage="10 weeks after germination"
/clone_lib="KS08"
/note="Vector: pBluescript SK(-)"

Alignment Scores:
Pred. No.: 0.00679 Length: 127
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-857-841-4 (1-14) x BM067231 (1-127)

QY 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
78 ATGACAAATCTGAATCAACGAGTGTGTGTAACCGTCGA 37

RESULT 2
BE023342/c 416 bp mRNA linear EST 24-JUL-2004
LOCUS sm70f09.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-c1028-9282 5' similar to TR:Q13437 Q13437 DELETED IN SPLIT
HAND/SPLIT FOOT 1 ;, mRNA sequence.

ACCESSION BE023342
VERSION BE023342.1 GI:8285783
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE 1 (bases 1 to 416)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Other_ESTs: BI971551 corresponding to Gm-r1083-4800 (3')
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 1035 Std Error: 0.00.

FEATURES
Source Location/Qualifiers
1..416
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Supernod"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1028-9282"
/tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
/clone_lib="Gm-c1028"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; The mRNA was isolated from roots of Glycine max
'Supernod' plants generously donated by Dr. Gary Stacey.
The seedlings were inoculated with Bradyrhizobium
japonicum, strain USDA110 prior to harvest. Stratagene's
cDNA synthesis kit (catalog number 200401) was used to

synthesize the cDNA. First-strand synthesis was performed
with 5-methyl dCTP, hence the ligated cDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An 'anchor'
nucleotide (V=A,C, or G) was added to the 3' end of the
primer [GAGAGAGAGAGAGAGAGACTAGTCTCGAG(T)18V] to anchor
the primer at the 5' end of the poly(A) tract. After
second-strand synthesis, the cDNA ends were filled in with
cloned Pfu DNA polymerase, ligated to EcoRI adapters and
subsequently phosphorylated. The XhoI site within the
first-strand synthesis primer was then restricted by
digestion with XhoI; all XhoI sites in the cDNA would be
protected by their hemimethylated status. The cDNA
constructs were size-fractionated with a 500bp cutoff,
using GibcoBRL Life Technologies' cDNA Size Fractionation
column. The column eluent was then ligated into
Stratagene's pBluescript II XR predigested vector
(pBluescript II SK(+)) that has been digested with EcoRI
and XhoI, and phosphorylated by Stratagene). Both the
white and blue colonies appear to contain recombinant
plasmids with cDNA inserts, based on size (n=25). This
library was constructed by Dr. Paul Keim and Dr. Virginia
Coryell."

ORIGIN

Alignment Scores:
Pred. No.: 92.7 Length: 416
Score: 49.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 71.01% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x BE023342 (1-416)

QY 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 123 ATGACAAAGCCGAACTACCGCGCTGTGAGAGAAAGAAAGA 82

RESULT 3
CA800884/c 443 bp mRNA linear EST 01-JUL-2004
LOCUS sat26b02.y1 Gm-c1056 Glycine soja cDNA clone SOYBEAN CLONE ID:
DEFINITION Gm-c1056-2379 5' similar to TR:Q9XIR8 Q9XIR8 F13011.6 PROTEIN. ;,
mRNA sequence.

ACCESSION CA800884
VERSION CA800884.1 GI:26057970
KEYWORDS EST.
SOURCE Glycine soja
ORGANISM Glycine soja
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE 1 (bases 1 to 443)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD

57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
1..443

/organism="Glycine soja"
/mol_type="mRNA"
/db_xref="taxon:3848"
/clone="SOYBEAN CLONE ID: Gm-c1056-2379"
/tissue_type="Whole seedling, 4 day old"
/lab_host="DH10B"
/clone_lib="Gm-c1056"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from 4 day old seedling of PI468916. The seedlings were germinated in a growth chamber using germination paper. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN
Alignment Scores:
Pred. No.: 98.8 Length: 443
Score: 49.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 71.01% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x CA800884 (1-443)

QY 1 MetAaplysSerGluSerThrSeraLaGlyArgAsnArgArg 14
|||||:::|||||:::|||||
Db 112 ATGGACAAAGCCGAATCTACCGGCTGTGGAAGACGAAAGA 71

RESULT 4
BI468772/c 456 bp mRNA linear EST 08-JUL-2004
LOCUS
DEFINITION
ID: Gm-c1050-4363 5' similar to TR:Q9XIR8 Q9XIR8 F13011.6 PROTEIN.
', mRNA sequence.

ACCESSION
BI468772
VERSION
BI468772.1 GI:15284890
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE
1 (bases 1 to 456)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project

TITLE
JOURNAL
COMMENT
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this

clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 360.
Location/Qualifiers
1..456

/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Clark"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1050-4363"
/tissue_type="leaf tissue at various developmental stages of greenhouse grown plants"
/dev_stage="3 week old"
/lab_host="DH10B"
/clone_lib="Gm-c1050"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The Clark NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from leaf tissue at various developmental stages of 3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."

ORIGIN
Alignment Scores:
Pred. No.: 102 Length: 456
Score: 49.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 71.01% Indels: 0
DB: 4 Gaps: 0

US-09-857-841-4 (1-14) x BI468772 (1-456)

QY 1 MetAaplysSerGluSerThrSeraLaGlyArgAsnArgArg 14
|||||:::|||||:::|||||
Db 85 ATGGACAAAGCCGAATCTACCGGCTGTGGAAGACGAAAGA 44

RESULT 5
BI971551 544 bp mRNA linear EST 23-OCT-2001
LOCUS
DEFINITION
ID: Gm-r1083 Glycine max cDNA clone Gm-r1083-4800 3', mRNA sequence.

ACCESSION
BI971551
VERSION
BI971551.1 GI:16345956
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE
1 (bases 1 to 544)
Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Coryell,V., Erpelding,J., Rapp,C., Shoop,E., Pardinas,J., Liu,L. and Lewin,H.
A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)
Other ESTs: BE023342 corresponding to Gm-c1028-9282 (5')
Contact: Vodkin,L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics
University of Illinois

TITLE
JOURNAL
COMMENT
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this

Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4582
Email: l-vodkin@uiuc.edu
This clone is available through: Incyte Genomics, 4633 World
Parkway Circle St. Louis, Missouri 63134. Phone (800) 430-0030 or
(314) 427-3222 FAX: (314) 427-3324. Web site:
<http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboratio>
[n/index](http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboratio)
Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'.

FEATURES

Source
Location/Qualifiers

1..544
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="Gm-r1083-4800"
/clone_lib="Gm-r1083"
/note="The library Gm-r1083 is a sequence-driven, reracked
set of 4,992 clones selected from cDNA libraries from
various tissues and stages of development of soybean. It
represents 1117 sequences from the progenitor library
Gm-cl009 (from mature roots of 2 month old greenhouse
grown 'Williams' soybean plants); 820 sequences from the
progenitor library Gm-cl013 (from 2 to 3 week old whole
plants of Williams); and 3055 sequences from library
Gm-cl028 (from 'Supernod' plants whose seedlings were
inoculated with *Bradyrhizobium japonicum*, courtesy of Dr.
Gary Stacey). The 5' ESTs of the source clones from the
different progenitor libraries was used to select
singletons, or a representative of each contig, which were
reracked to form library Gm-r1083. The cDNA clones of the
reracked Gm-r1083 library were then sequenced at the 3'
end. The contig analysis to select unique genes was
performed by the laboratory of Ernest Retzel, Center for
Computational Genomics and Bioinformatics, University of
Minnesota, <http://web.ahc.umn.edu/biodata/nsfsou/>.
Reracking was performed by Incyte Genomics, St. Louis,
<http://www.incyte.com>, and 3' sequencing by the Keck
Center for Comparative and Functional Genomics, University
of Illinois, <http://www.lie.uiuc.edu/biotech/keck.html>.
Note: The corresponding 5' EST from each clone in the
Gm-r1083 library is listed in the 'OTHER EST' field. The
detailed information on the source library for each clone
can also be obtained by referring to the Incyte Genomics
clone ID of the original cDNA library that is also listed
under 'OTHER EST'."

ORIGIN

Alignment Scores:

Pred. No.:	122	Length:	544
Score:	49.00	Matches:	9
Percent Similarity:	78.57%	Conservative:	2
Best Local Similarity:	64.29%	Mismatches:	3
Query Match:	71.01%	Indels:	0
DB:	4	Gaps:	0

US-09-857-841-4 (1-14) x BI971551 (1-544)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||:::|||||:::|||||
Db 421 ATGCACAAAGCCGAATCTACCGCTGTGGAAGAACGAAGAAGA 462

RESULT 6

AQ737846 617 bp DNA linear GSS 16-JUL-1999
LOCUS AQ737846
DEFINITION HS_2167_A1_B08_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2167 Col=15 Row=C, genomic survey
sequence.

ACCESSION AQ737846
VERSION AQ737846.1 GI:5515368
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
10449764
Contact: Mahairas GC, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 2167 row: C column: 15
Seq primer: T7
Class: BAC ends
High quality sequence stop: 617.
Location/Qualifiers

FEATURES

Source

1..617
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2167 Col=15 Row=C"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN

Alignment Scores:

Pred. No.:	210	Length:	617
Score:	48.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	6
Best Local Similarity:	57.14%	Mismatches:	0
Query Match:	69.57%	Indels:	0
DB:	8	Gaps:	0

US-09-857-841-4 (1-14) x AQ737846 (1-617)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
:::||||:::|||||:::|||||
Db 596 ATAGATCAAAATGATCAAGCTCAAGCGCCGCTAATAAGAGG 555

RESULT 7

CC978898 956 bp DNA linear GSS 18-AUG-2003
LOCUS CC978898
DEFINITION ZUAG628TH_ZM_3_0_4_0_KB Zea mays genomic clone ZMMPBa0057F07,
genomic survey sequence.

ACCESSION CC978898
VERSION CC978898.1 GI:33838776
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 956)
Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: ZUAG628TV
Contact: Cathy Whiteley

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source
1..956
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMPa0057F07"
/clone_lib="ZM_3.0_4.0_KB"
/note="Vector: pBCSK-; site_1: HincII; 3-4 kb 'unfiltered'
genomic DNA library"

ORIGIN
Alignment Scores:
Pred. No.: 329
Score: 48.00
Percent Similarity: 85.71%
Best Local Similarity: 57.14%
Query Match: 69.57%
DB: 9
Length: 956
Matches: 8
Conservative: 4
Mismatches: 2
Indels: 0
Gaps: 0

US-09-857-841-4 (1-14) x CC978898 (1-956)

QY 1 MetAspIySergIuSerThrSerAlaGlyArgAsnArgArg 14
:::|||||:::|||||
Db 213 CTGCACAAGACGAGCAGCCGCTGGGAAGAAACGGCGG 172

RESULT 8
LOCUS CF568862 594 bp mRNA linear EST 23-SEP-2003
DEFINITION FAMU USDA FP 00084 Vitis shuttleworthii L., grape Vitis
shuttleworthii cDNA 5', mRNA sequence.
ACCESSION CF568862
VERSION CF568862.1 GI:34994945
KEYWORDS EST.
SOURCE Vitis shuttleworthii
ORGANISM Vitis shuttleworthii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 594)
Hunter,W.B., Dang,P.M., Chaparro,J.X., Lu,J. and Leong,S.
Genes expressed in Vitis shuttleworthii L
Unpublished (2004)
Contact: Jiang Lu, FAMU, Wayne Hunter, USDA,ARS
Viticulture Centre, FAMU, Tallahassee, FL
Florida A&M University
Tallahassee, FL 32317, USA
Tel: (850) 412-7393
Fax: (850) 561-2617, (772) 462-5898
Email: jiang.lu@fam.u.edu,
Seq primer: T3 Primer.

FEATURES
source
1..594
/organism="Vitis shuttleworthii"
/mol_type="mRNA"
/db_xref="taxon:246827"
/sex="Mixed population"
/tissue_type="Entire tendril, leaves, bud, flowers"
/dev_stage="At blooming"
/lab_host="XJ1-Blue"
/clone_lib="Vitis shuttleworthii L., grape"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; A high quality EST with at least 100 contiguous
bases at Trace Tuner score of 20 or better. Construction
by PM Dang, USDA, ARS, U.S. Horticultural Research Lab,
Ft. Pierce, FL, USA."

ORIGIN

Alignment Scores:
Pred. No.: 306
Score: 47.00
Percent Similarity: 100.00%
Best Local Similarity: 81.82%
Query Match: 68.12%
DB: 7
Length: 594
Matches: 9
Conservative: 2
Mismatches: 0
Indels: 0
Gaps: 0

US-09-857-841-4 (1-14) x CF568862 (1-594)

QY 4 SergIuSerThrSerAlaGlyArgAsnArgArg 14
:::|||||:::|||||
Db 73 ACAGAGACAACATCTGCAGGAGAAATCGGAGA 105

RESULT 9
LOCUS AL584972 413 bp mRNA linear EST 28-FEB-2001
DEFINITION AL584972 Stratagene Chick Embryo Lambda cDNA Library (* 937405)
Gallus gallus cDNA clone ROS016G12, mRNA sequence.
ACCESSION AL584972
VERSION AL584972.1 GI:13163705
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 413)
Murray,F.
Stratagene Chick Embryo Lambda cDNA Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bsrc.ac.uk
Seq primer: T3.

FEATURES
source
1..413
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS016G12"
/tissue_type="Embryo"
/dev_stage="5 days old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene Chick Embryo Lambda cDNA Library (*
937405)"
/note="Vector: pBLUESCRIPT SK; Site 1: EcoRI; Site 2:
XhoI; cloned unidirectionally. Primer: Oligo dT. Uni-ZAP
XR vector. Average insert size: 1.5kb.; 5' adaptor
sequence: 5' GAATTCGGCAGAG 3'; 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3'."

ORIGIN

Alignment Scores:
Pred. No.: 320
Score: 46.00
Percent Similarity: 78.57%
Best Local Similarity: 64.29%
Query Match: 66.67%
DB: 1
Length: 413
Matches: 9
Conservative: 2
Mismatches: 3
Indels: 0
Gaps: 0

US-09-857-841-4 (1-14) x AL584972 (1-413)

QY 1 MetAspIySergIuSerThrSerAlaGlyArgAsnArgArg 14
:::|||||:::|||||
Db 267 ATACAGAAATCTGAAGTACAGCTCCTGGAACAACAGGCGG 226

RESULT 10
AL836204

LOCUS	AL836204	480 bp	mRNA	linear	EST 27-FEB-2004
DEFINITION	AL836204 EFRd Takifugu rubripes cDNA clone EFRd002apsA11, mRNA sequence.				
ACCESSION	AL836204				
VERSION	AL836204				
KEYWORDS	EST.				
SOURCE	Takifugu rubripes (Fugu rubripes)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Takifugu.				
REFERENCE	Clark,M.S., Edwards,Y.J., Peterson,D., Clifton,S.W., Thompson,A.J., Sasaki,M., Suzuki,Y., Kikuchi,K., Watabe,S., Kawakami,K., Sugano,S., Elgar,G. and Johnson,S.L. Fugu ESTs: new resources for transcription analysis and genome annotation Genome Res. 13 (12), 2747-2753 (2003)				
TITLE	JOURNAL COMMENT				
JOURNAL COMMENT	Contact: Clark MS MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB, UK Email: biohelp@hgmp.mrc.ac.uk Email: biohelp@hgmp.mrc.ac.uk Vector: pBluescript II KS V_type: phagemid PRIMER: KS The clone can be obtained from www.hgmp.mrc.ac.uk Library created by Greg Elgar MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK Library sequenced by Sarah Warner and Jim Hills MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK.				
FEATURES	Location/Qualifiers 1..480 /organism="Takifugu rubripes" /mol_type="mRNA" /db_xref="taxon:31033" /clone="EFRd002apsA11" /tissue_type="gut" /clone_lib="EFRd" /note="Vector: pBluescript II KS"				
ORIGIN	Alignment Scores: Pred. No.: 373 Length: 480 Score: 46.00 Matches: 10 Percent Similarity: 76.92% Conservative: 0 Best Local Similarity: 76.92% Mismatches: 3 Query Match: 66.67% Indels: 0 DB: 1 Gaps: 0				
US-09-857-841-4 (1-14) x AL836204 (1-480)					
OY	2 AsplysergluSerThrserAlaglyArgAsnargArg 14 Db 397 GATGGAGCGAATCGAACGCCTGACGTGACGACGA 435				
RESULT 11					
LOCUS	BX256743	486 bp	mRNA	linear	EST 24-MAY-2004
DEFINITION	BX256743 AGENAE Gallus gallus multi-tissues normalized library (gcag) Gallus gallus CDNA clone gcag0001c.c.05 5prim, mRNA sequence.				
ACCESSION	BX256743				
VERSION	BX256743.2 GI:47581535				
KEYWORDS	EST.				
SOURCE	Gallus gallus (chicken)				
ORGANISM	Gallus gallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.				

REFERENCE	1 (bases 1 to 486)
AUTHORS	Herault,F., Le Meuth-Metzinger,V., Desert,C., Retout,E., Plumi,F., Klomp,C. and Douaire,M.
TITLE	Construction and primary characterization of chicken normalized multi-tissue cDNA libraries
JOURNAL	Unpublished (2003)
COMMENT	On Feb 27, 2003 this sequence version replaced gi:28579341.
	Contact: Douaire M
	INRA, UMR INRA-ENSAR Genetique Animale
	65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE
	Tel: +33 (0) 2.23.48.54.63
	Fax: +33 (0) 2.23.48.54.70
	Email: Madeleine.Douaire@roazhon.inra.fr
	Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenassupport@jouy.inra.fr to obtain the chromatogram of this sequence.
	Plate: 0001 row: c column: 5
	Seq primer: M13R.
FEATURES	
source	Location/Qualifiers
	1..486
	/organism="Gallus gallus"
	/mol_type="mRNA"
	/db_xref="taxon:9031"
	/clone="gcag0001c.c.05"
	/tissue_type="multi-tissues"
	/dev_stage="from embryos to adults"
	/lab_host="DH10B"
	/clone_lib="AGENAE Gallus gallus multi-tissues normalized library (gcag)"
	/note="Vector: pT7T3D-pac; tissues: brain, embryos, kidney, multi-tissues, muscle, pancreas, skin, testis, liver, adipose tissue, granulosa, utero-vaginal gland, oviduct, small follicle, ovary, hypothalamus, pituitary gland, ileon, jejunum, caecum, duodenum, spleen, fabricius gland, bone marrow, thymus, hematopoietic progenitor cells. Clone distribution : AGENAE Resource centre. Francois PIUMI, Francois.Piumi.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"
ORIGIN	
Alignment Scores:	
Pred. No.:	378
Score:	46.00
Percent Similarity:	78.57%
Best Local Similarity:	64.29%
Query Match:	66.67%
DB:	5
	Matches: 9
	Conservative: 2
	Mismatches: 3
	Indels: 0
	Gaps: 0
US-09-857-841-4 (1-14) x BX256743 (1-486)	
Qy	1 MetAspIysSerGlnSerThrSerAlaGlyArgAsnArgArg 14
	::: :::
Db	71 ATACAGAAATCTGAAAGTACAGCTCCTGGAACACAGCGG 30
RESULT 12	
BX256742/c	490 bp mRNA linear EST 24-MAY-2004
LOCUS	BX256742 AGENAE Gallus gallus multi-tissues normalized library
DEFINITION	(gcag) Gallus gallus cDNA clone gcag0001c.c.05 3prim, mRNA
	sequence.
ACCESSION	BX256742
VERSION	BX256742.2 GI:47581534
KEYWORDS	EST.
SOURCE	Gallus gallus (chicken)
ORGANISM	Gallus gallus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE	1 (bases 1 to 490)
AUTHORS	Herault,F., Le Meuth-Metzinger,V., Desert,C., Retout,E., Plumi,F., Klomp,C. and Douaire,M.
TITLE	Construction and primary characterization of chicken normalized

JOURNAL COMMENT

multi-tissue cDNA libraries
Unpublished (2003)
On Feb 27, 2003 this sequence version replaced gi:28579340.
Contact: Douaire M
INRA, UMR INRA-ENSAR Genetique Animale
65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE
Tel: +33 (0) 2.23.48.54.63
Fax: +33 (0) 2.23.48.54.70
Email: Madeleine.Douaire@roazhon.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenassupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0001 row: c column: 5
Seq primer: M13P.

FEATURES source

Location/Qualifiers
1. 490
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="gcag0001c.c.05"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="AGENAE Gallus gallus multi-tissues normalized
library (gcag)"
/note="Vector: pT7T3D-pac; tissues: brain, embryos,
kidney, multi-tissues, muscle, pancreas, skin, testis,
liver, adipose tissue, granulosa, utero-vaginal gland,
oviduct, small follicle, ovary, hypothalamus, pituitary
gland, ileon, jejunum, caecum, duodenum, spleen,
fabricius gland, bone marrow, thymus, hematopoietic
progenitor cells. Clone distribution : AGENAE Resource
centre. Francois Piumi, Francois.Piumi.inra.fr, INRA, CEA
Radiobiologie et Etude du genome (LREG), Domaine de
Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"

ORIGIN

Alignment Scores:
Pred. No.: 381 Length: 490
Score: 46.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 66.67% Indels: 0
DB: 5 Gaps: 0

US-09-857-841-4 (1-14) x BX256742 (1-490)

QY 1 MetAsplySerGluSerThrSerAlaGlyArgAsnArgArg 14
::: ||||| ||||| ::||| |||||
Db 71 ATACAGAAATCTGAAGTACAGCTCTGGAACAACAGCGCG 30

RESULT 13

CD356033 645 bp mRNA linear EST 29-MAY-2003
LOCUS AGENCOURT 14292133 NIH_MGC_176 Mus musculus cDNA clone
DEFINITION IMAGE:30379119 5', mRNA sequence.
ACCESSION CD356033
VERSION CD356033.1 GI:31127444
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 645)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein

JOURNAL COMMENT

CDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: NDCM169 row: a column: 16
High quality sequence stop: 258.
Location/Qualifiers
1. 645
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30379119"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_176"
/note="Organ: kidney; Vector: pDNR-LIB; Site 1: SfiI
(ggccatattggcc); Site 2: SfiI (ggccgctcgcc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGACGAGCGCATTCAGCGCGG-3' and
5'-ATTCTAGAGCCCGAGGCGGCCACATG-dt(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

FEATURES source

Alignment Scores:
Pred. No.: 505 Length: 645
Score: 46.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 66.67% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x CD356033 (1-645)

QY 1 MetAsplySerGluSerThrSerAlaGlyArgAsnArgArg 14
::: ||||| ||||| ::||| |||||
Db 112 CTTCAAAACAAGACGGGTTCTGCTGGAGAAACCGCGCA 153

RESULT 14

CF577172 653 bp mRNA linear EST 24-SEP-2003
LOCUS MCSA209G04 Maturing Sugarcane Stem Lambda ZIPLOX Library (MCS)
DEFINITION Saccharum sp. cDNA clone MCSA189F12 5', mRNA sequence.
ACCESSION CF577172
VERSION CF577172.1 GI:35208498
KEYWORDS EST.
SOURCE Saccharum sp.
ORGANISM Saccharum sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 653)
Casu, R.B., Dimmock, C.M., Chapman, S.C., Grof, C.P.L., McIntyre, C.L.,
Bonnett, G.D. and Manners, J.M.
Identification of differentially expressed transcripts from
maturing stem of sugarcane by in silico analysis of stem expressed
sequence tags and gene expression profiling
Unpublished (2003)
Contact: Rosanne E. Casu
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
Long Pocket Laboratories, 120 Meiers Rd, Indooroopilly, QLD, 4068,
Australia
Tel: 61 7 3214 2364
Fax: 61 7 3214 2881
Email: Rosanne.Casu@csiro.au
Bases 1-17 (GTGACCCACGCGTCG): Sail adapter
Seq primer: T7 sequencing primer
High quality sequence stop: 655.

JOURNAL COMMENT

FEATURES
Source
Location/Qualifiers
1..653
/organism="Saccharum sp."
/mol_type="mRNA"
/cuiivar="Q117"
/db_xref="taxon:15819"
/clone="MCSA189F12"
/dev_stage="12 months post-planting"
/lab_host="Y1090(ZL)"
/clone_lib="Maturing Sugarcane Stem Lambda ZIPLOX library (MCS)"
/note="Organ: internodes 6-11; Vector: Lambda ZIPLOX; Site_1: Sali; Site_2: NotI; mRNA was prepared from internodes 6-11 of the sugarcane variety Q117. cDNA was synthesised from a NotI-oligodT primer/adaptor using the manufacturers protocols (Life Technologies) and then ligated to a Sali adaptor to facilitate directional cloning. The cDNA was cloned into the Sali and NotI sites of the Lambda ZIPLOX phage vector (Life Technologies). Constructed by Rosanne E. Casu."

ORIGIN
Alignment Scores:
Pred. No.: 511 Length: 653
Score: 46.00 Matches: 9
Percent Similarity: 85.71% Conservative: 3
Best Local Similarity: 64.29% Mismatches: 2
Query Match: 66.67% Indels: 0
DB: 7 Gaps: 0

US-09-857-841-4 (1-14) x CF577172 (1-653)

QY 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArg 14
:::|||||:::|||||
Db 245 CTTGACAAAGCGAGAGACGACGACGAGAGAGAGAGAG 286

RESULT 15
AG540710/c
LOCUS AG540710 677 bp DNA linear GSS 05-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-453M10.TJ, genomic survey sequence.
ACCESSION AG540710
VERSION AG540710.1 GI:48301124
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 677)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES
Source
Location/Qualifiers
1..677
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-453M10.TJ"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC library"

ORIGIN
Alignment Scores:
Pred. No.: 530 Length: 677
Score: 46.00 Matches: 9
Percent Similarity: 71.43% Conservative: 1
Best Local Similarity: 64.29% Mismatches: 4
Query Match: 66.67% Indels: 0
DB: 9 Gaps: 0

US-09-857-841-4 (1-14) x AG540710 (1-677)

QY 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArg 14
|||:::|||||
Db 284 ATGAACAAAGGAGCAAGTAGAGGACGAGCAAGCAAGA 243

Search completed: December 5, 2004, 09:41:17
Job time : 2049 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 08:19:02 ; Search time 67 Seconds
(without alignments)
148.523 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSAGRNR 14

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 segs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09857841/runat_03122004_160552_18608/app_query.fasta_1.199
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09857841@cgn_1_1_69@runat_03122004_160552_18608 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	130	1	US-08-090-193-14 Sequence 14, Appl
2	69	100.0	130	2	US-08-488-031-14 Sequence 14, Appl
3	69	100.0	130	2	US-08-486-569-14 Sequence 14, Appl
4	69	100.0	130	2	US-08-488-027-14 Sequence 14, Appl
5	69	100.0	130	2	US-08-090-192-14 Sequence 14, Appl
6	69	100.0	130	2	US-08-482-663-14 Sequence 14, Appl
7	69	100.0	130	3	US-08-482-658-14 Sequence 14, Appl
8	69	100.0	130	3	US-08-470-349-14 Sequence 14, Appl
9	69	100.0	130	3	US-08-475-610-14 Sequence 14, Appl
10	69	100.0	130	5	PCT-US92-00277-14 Sequence 14, Appl
11	69	100.0	130	5	PCT-US92-00278-14 Sequence 14, Appl
12	69	100.0	131	1	US-08-090-193-11 Sequence 11, Appl

13	69	100.0	131	2	US-08-488-031-11	Sequence 11, Appl
14	69	100.0	131	2	US-08-486-569-11	Sequence 11, Appl
15	69	100.0	131	2	US-08-488-027-11	Sequence 11, Appl
16	69	100.0	131	2	US-08-090-192-11	Sequence 11, Appl
17	69	100.0	131	2	US-08-482-663-11	Sequence 11, Appl
18	69	100.0	131	3	US-08-482-658-11	Sequence 11, Appl
19	69	100.0	131	3	US-08-470-349-11	Sequence 11, Appl
20	69	100.0	131	3	US-08-475-610-11	Sequence 11, Appl
21	69	100.0	131	5	PCT-US92-00277-11	Sequence 11, Appl
22	69	100.0	131	5	PCT-US92-00278-11	Sequence 11, Appl
23	69	100.0	152	1	US-08-090-193-9	Sequence 9, Appl
24	69	100.0	152	1	US-08-090-193-10	Sequence 9, Appl
25	69	100.0	152	2	US-08-488-031-9	Sequence 9, Appl
26	69	100.0	152	2	US-08-488-031-10	Sequence 9, Appl
27	69	100.0	152	2	US-08-486-569-9	Sequence 9, Appl
28	69	100.0	152	2	US-08-486-569-10	Sequence 9, Appl
29	69	100.0	152	2	US-08-488-027-9	Sequence 9, Appl
30	69	100.0	152	2	US-08-488-027-10	Sequence 9, Appl
31	69	100.0	152	2	US-08-090-192-9	Sequence 9, Appl
32	69	100.0	152	2	US-08-090-192-10	Sequence 9, Appl
33	69	100.0	152	2	US-08-482-663-9	Sequence 9, Appl
34	69	100.0	152	2	US-08-482-663-10	Sequence 9, Appl
35	69	100.0	152	3	US-08-482-658-9	Sequence 9, Appl
36	69	100.0	152	3	US-08-482-658-10	Sequence 9, Appl
37	69	100.0	152	3	US-08-470-349-9	Sequence 9, Appl
38	69	100.0	152	3	US-08-470-349-10	Sequence 9, Appl
39	69	100.0	152	3	US-08-475-610-9	Sequence 9, Appl
40	69	100.0	152	3	US-08-475-610-10	Sequence 9, Appl
41	69	100.0	152	5	PCT-US92-00277-9	Sequence 9, Appl
42	69	100.0	152	5	PCT-US92-00277-10	Sequence 9, Appl
43	69	100.0	153	5	PCT-US92-00278-10	Sequence 10, Appl
44	69	100.0	153	5	PCT-US92-00278-12	Sequence 12, Appl
45	69	100.0	154	1	US-08-090-193-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-090-193-14
; Sequence 14, Application US/08090193
; Patent No. 5641673
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perrimon, No. 5641673bert
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESS: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090,193
; FILING DATE: 23-DEC-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0609.3080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-090-193-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-857-841-4 (1-14) x US-08-090-193-14 (1-130)

QY 1 MetaspysSerGluserThrsEraLaGlyArgAsnArgArg 14
Db 53 ATGGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 94

RESULT 2
US-08-488-031-14
Sequence 14, Application US/08488031
Patent No. 5849548
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5849548bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,031
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080002/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both

TOPOLOGY: linear
US-08-488-031-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-031-14 (1-130)

QY 1 MetaspysSerGluserThrsEraLaGlyArgAsnArgArg 14
Db 53 ATGGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 94

RESULT 3
US-08-486-569-14
Sequence 14, Application US/08486569
Patent No. 5863774
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5863774bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,569
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080006/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-486-569-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-486-569-14 (1-130)

QY 1 MetAspLySergIuSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 53 ATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTGA 94

RESULT 4

US-08-488-027-14

; Sequence 14, Application US/08488027

; Patent No. 5866384

; GENERAL INFORMATION:

; APPLICANT: Haseloff, James

; APPLICANT: Brand, Andrea

; APPLICANT: Perrimon, No. 5866384bert

; APPLICANT: Goodman, Howard M.

; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, N.W., Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,027

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/090,193

; FILING DATE: 23-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00277

; FILING DATE: 16-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/642,330

; FILING DATE: 17-JAN-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Bugalsky, Lawrence B.

; REGISTRATION NUMBER: 35,086

; REFERENCE/DOCKET NUMBER: 0609.3080003/MAC/LBB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 130 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; US-08-488-027-14

Alignment Scores:

Pred. No.: 0.00013

Score: 69.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 2

Length: 130

Matches: 14

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-027-14 (1-130)

QY 1 MetAspLySergIuSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 53 ATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTGA 94

RESULT 5

US-08-090-192-14

; Sequence 14, Application US/08090192

; Patent No. 5874414

; GENERAL INFORMATION:

; APPLICANT: Haseloff, James

; APPLICANT: Goodman, Howard M.

; TITLE OF INVENTION: Trans-Splicing Ribozymes

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/090,192

; FILING DATE: 11-NOV-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/ US 92/00278

; FILING DATE: 16-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/642,333

; FILING DATE: 17-JAN-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Cimbala, Michele A.

; REGISTRATION NUMBER: 33,851

; REFERENCE/DOCKET NUMBER: 0609.3030001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 130 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: both

; US-08-090-192-14

Alignment Scores:

Pred. No.: 0.00013

Score: 69.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 2

Length: 130

Matches: 14

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-857-841-4 (1-14) x US-08-090-192-14 (1-130)

QY 1 MetAspLySergIuSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 53 ATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTGA 94

RESULT 6

US-08-482-663-14

; Sequence 14, Application US/08482663

; Patent No. 5882907

; GENERAL INFORMATION:

; APPLICANT: Haseloff, James

; APPLICANT: Brand, Andrea

; APPLICANT: Perrimon, No. 5882907bert

; APPLICANT: Goodman, Howard M.

; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,663
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080005/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-482-663-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-482-663-14 (1-130)

QY 1 MetAsplysSerGluSerThrSeraIaGlyArgAsnArg 14
Db 53 ATGGACAAATCTGATCAACCAAGTGTGTCGTACCGTCGA 94

RESULT 7
US-08-482-658-14
Sequence 14, Application US/08482658
Patent No. 6010904
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 6010904bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080008/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-482-658-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-857-841-4 (1-14) x US-08-482-658-14 (1-130)

QY 1 MetAsplysSerGluSerThrSeraIaGlyArgAsnArg 14
Db 53 ATGGACAAATCTGATCAACCAAGTGTGTCGTACCGTCGA 94

RESULT 8
US-08-470-349-14
Sequence 14, Application US/08470349
Patent No. 6015794
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,349
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,192
FILING DATE: 11-NOV-1993
APPLICATION NUMBER: PCT/ US 92/00278
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,333

FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalá, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-470-349-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-857-841-4 (1-14) x US-08-470-349-14 (1-130)

QY 1 MetAplysSergluserThrsAlaGlyArgAsnArgArg 14
Db 53 ATGCACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGA 94

RESULT 9
US-08-475-610-14
Sequence 14, Application US/08475610
Patent No. 6071730
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 6071730bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,610
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080004/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-475-610-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-857-841-4 (1-14) x US-08-475-610-14 (1-130)

QY 1 MetAplysSergluserThrsAlaGlyArgAsnArgArg 14
Db 53 ATGCACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGA 94

RESULT 10
PCT-US92-00277-14
Sequence 14, Application PC/TUS9200277
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, Norbert
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 19920116
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3496604
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 833-7533
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US92-00277-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-857-841-4 (1-14) x PCT-US92-00277-14 (1-130)

OY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 53 ATGCACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 94

RESULT 11

PCT-US92-00278-14

; Sequence 14, Application PC/TUS9200278

; GENERAL INFORMATION:

; APPLICANT: Haseloff, James

; APPLICANT: Goodman, Howard M.

; TITLE OF INVENTION: Trans-Splicing Ribozymes

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1225 Connecticut Avenue, N.W., Suite 300

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00278

; FILING DATE: 19920116

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/642,333

; FILING DATE: 17-JAN-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Goldstein, Jorge A

; REGISTRATION NUMBER: 29,021

; REFERENCE/DOCKET NUMBER: 0609.3476604

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 833-7533

; TELEFAX: (202) 833-8716

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 130 bases

; TYPE: NUCLEIC ACID

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; MOLECULE TYPE: Nucleic Acid

PCT-US92-00278-14

Alignment Scores:

Pred. No.: 0.00013

Score: 69.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 5

US-09-857-841-4 (1-14) x PCT-US92-00278-14 (1-130)

OY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 53 ATGCACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 94

RESULT 12

US-08-090-193-11

; Sequence 11, Application US/08090193

; Patent No. 5641673

; GENERAL INFORMATION:

; APPLICANT: Haseloff, James

; APPLICANT: Brand, Andrea

; APPLICANT: Perrimon, No. 5641673bert

; APPLICANT: Goodman, Howard M.

; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/090,193

; FILING DATE: 23-DEC-1993

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00277

; FILING DATE: 16-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/642,330

; FILING DATE: 17-JAN-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Cimbala, Michele A.

; REGISTRATION NUMBER: 33,851

; REFERENCE/DOCKET NUMBER: 0609.3080001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 131 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: both

US-08-090-193-11

Alignment Scores:

Pred. No.: 0.000131

Score: 69.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 1

US-09-857-841-4 (1-14) x US-08-090-193-11 (1-131)

OY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
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Db 54 ATGCACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 95

RESULT 13

US-08-488-031-11

; Sequence 11, Application US/08488031

; Patent No. 5849548

; GENERAL INFORMATION:

; APPLICANT: Haseloff, James

; APPLICANT: Brand, Andrea

; APPLICANT: Perrimon, No. 5849548bert

; APPLICANT: Goodman, Howard M.

; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, N.W., Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,031
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080002/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-488-031-11

Alignment Scores:
Pred. No.: 0.000131 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-031-11 (1-131)

QY 1 MetAsplysSerGluSerThrSerAlaGlyArgAsnArgArg 14
DB 54 ATGACCAATCTGATCAACCACTGCTGCTGTAACCGTCGA 95

RESULT 14

US-08-486-569-11

; Sequence 11, Application US/08486569

; Patent No. 5863774

; GENERAL INFORMATION:

; APPLICANT: Haseloff, James

; APPLICANT: Brand, Andrea

; APPLICANT: Perrimon, No. 5863774bert

; APPLICANT: Goodman, Howard M.

; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, N.W., Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/486,569

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/090,193

; FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080006/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-486-569-11

Alignment Scores:
Pred. No.: 0.000131 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-486-569-11 (1-131)

QY 1 MetAsplysSerGluSerThrSerAlaGlyArgAsnArgArg 14
DB 54 ATGACCAATCTGATCAACCACTGCTGCTGTAACCGTCGA 95

RESULT 15

US-08-488-027-11

; Sequence 11, Application US/08488027

; Patent No. 5866384

; GENERAL INFORMATION:

; APPLICANT: Haseloff, James

; APPLICANT: Brand, Andrea

; APPLICANT: Perrimon, No. 5866384bert

; APPLICANT: Goodman, Howard M.

; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, N.W., Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,027

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/090,193

; FILING DATE: 23-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00277

; FILING DATE: 16-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/642,330

; FILING DATE: 17-JAN-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Bugaisky, Lawrence B.

; REGISTRATION NUMBER: 35,086

/ REFERENCE/DOCKET NUMBER: 0609.3080003/MAC/LBB
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 131 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
US-08-488-027-11

Alignment Scores:
Pred. No.: 0.000131 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-027-11 (1-131)

QY 1 MetAspLybSerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 54 ATGACACAAATCTGAATCAACCAAGTGTGTGTAACCGTCGA 95

Search completed: December 5, 2004, 09:48:23
Job time : 68 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 08:17:52 ; Search time 350 Seconds
(without alignments)
219.793 Million cell updates/sec

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Perfect score: 69
Sequence: 1 MDKSESTSGRNRR 14

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Searched: 3694831 segs, 2747406616 residues

Total number of hits satisfying chosen parameters: 7389662

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	69	100.0	772	13	US-10-011-033-14	Sequence 14, Appli
4	69	100.0	792	13	US-10-011-033-3	Sequence 3, Appli
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6	48	69.6	3048	18	US-10-425-115-176381	Sequence 176381,
7	47	68.1	609	17	US-10-437-963-2533	Sequence 2533, Ap
8	47	68.1	792	17	US-10-437-963-3120	Sequence 3120, Ap
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10	44	63.8	568	17	US-10-437-963-49610	Sequence 49610, A
11	44	63.8	571	17	US-10-437-963-92187	Sequence 92187, A
12	44	63.8	615	17	US-10-437-963-64563	Sequence 64563, A
13	44	63.8	1603	16	US-10-282-122A-26385	Sequence 26385, A
14	44	63.8	2625	16	US-10-282-122A-28450	Sequence 28450, A
15	43	62.3	969	17	US-10-437-963-86635	Sequence 86635, A
16	43	62.3	1014	17	US-10-437-963-64807	Sequence 64807, A
17	43	62.3	2377	18	US-10-425-115-176349	Sequence 176349,
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26	42	60.9	610	13	US-10-027-632-717	Sequence 717, App
27	42	60.9	610	15	US-10-027-632-717	Sequence 717, App
28	42	60.9	889	17	US-10-424-599-34410	Sequence 34410, A
29	42	60.9	1058	16	US-10-424-599-113581	Sequence 113581,
30	42	60.9	1068	17	US-10-437-963-93102	Sequence 93102, A
31	42	60.9	1073	18	US-10-425-115-20144	Sequence 20144, A
32	42	60.9	1267	16	US-10-305-720-1267	Sequence 1267, Ap
33	42	60.9	1506	17	US-10-437-963-97456	Sequence 97456, A
34	42	60.9	1746	13	US-10-001-843-35	Sequence 35, Appli
35	42	60.9	1825	17	US-10-437-963-93100	Sequence 93100, A
36	42	60.9	1942	10	US-09-800-274-1	Sequence 1, Appli
37	42	60.9	2980	15	US-10-225-567A-23	Sequence 23, Appli
38	42	60.9	2983	17	US-10-741-601-5720	Sequence 5720, Ap
39	41.5	60.1	2508	17	US-10-437-963-60204	Sequence 60204, A
40	41	59.4	243	17	US-10-437-963-89248	Sequence 89248, A
41	41	59.4	289	9	US-09-294-093B-1361	Sequence 1361, Ap
42	41	59.4	385	18	US-10-425-115-134580	Sequence 134580,
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ALIGNMENTS

RESULT 1
US-10-011-033-5
; Sequence 5, Application US/10011033
; Publication No. US20020124286A1
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; McMaster, J. Russell
; Tricoli, David M
; Reynolds, John F
; Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; Cucumber Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber mosaic virus
STRAIN: V-34
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
OTHER INFORMATION: /codon start= 3
/function= "ENCAPSIDATES VIRUS RNA"
/product= "COAT PROTEIN"
/gene= "CP"
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US-10-011-033-5
Alignment Scores:
Pred. No.: 0.00072 Length: 771
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-5 (1-771)
QY 1 MetAspIysSerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 3 ATGGACAAATCTGAATCAACCAAGTGTCTGTAACCGTCGA 44
RESULT 2
US-10-011-033-1
Sequence 1, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: V-27
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-011-033-1
Alignment Scores:
Pred. No.: 0.000721 Length: 772
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-1 (1-772)
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Db 3 ATGGACAAATCTGAATCAACCAAGTGTCTGTAACCGTCGG 44
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US-10-011-033-14
Sequence 14, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: A35
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-011-033-14
Alignment Scores:
Pred. No.: 0.000721 Length: 772
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-14 (1-772)
QY 1 MetAspLySergLuserThrSerAlaGlyArgAsnArgArg 14
Db 3 ATGGACAAATCTGAATCAACCACTGCTGTCGTAACCGTCGA 44
RESULT 4
US-10-011-033-3
Sequence 3, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: V-33
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-011-033-3
Alignment Scores:
Pred. No.: 0.000741 Length: 792
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-3 (1-792)
QY 1 MetAspLySergLuserThrSerAlaGlyArgAsnArgArg 14
Db 3 ATGGACAAATCTGAATCAACCACTGCTGTCGTAACCGTCGA 44
RESULT 5
US-10-011-033-9
Sequence 9, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: CUCUMBER MOSAIC VIRUS
; STRAIN: STRAIN C
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..658
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-011-033-9

Alignment Scores:
Pred. No.: 0.00827 Length: 960
Score: 64.00 Matches: 13
Percent Similarity: 92.86% Conservative: 0
Best Local Similarity: 92.86% Mismatches: 1
Query Match: 92.75% Indels: 0
DB: 13 Gaps: 0

US-09-857-841-4 (1-14) x US-10-011-033-9 (1-960)

OY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
Db 1 ATGGACAAATCTGAATCAACCACTGCTGCTGTAACCATCGA 42

RESULT 6

US-10-425-115-176381
; Sequence 176381, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 176381
; LENGTH: 3048
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_92452C.1
US-10-425-115-176381

Alignment Scores:
Pred. No.: 32.9 Length: 3048
Score: 48.00 Matches: 8
Percent Similarity: 85.71% Conservative: 4
Best Local Similarity: 57.14% Mismatches: 2
Query Match: 69.57% Indels: 0
DB: 18 Gaps: 0

US-09-857-841-4 (1-14) x US-10-425-115-176381 (1-3048)

OY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
Db 1034 CTGACACAGACGAGACCGCGCTGGGAAGAAACCGCGG 1075

RESULT 7
US-10-437-963-2533/c
; Sequence 2533, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 2533
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102297C.1
US-10-437-963-2533

Alignment Scores:
Pred. No.: 9.37 Length: 609
Score: 47.00 Matches: 9
Percent Similarity: 84.62% Conservative: 2
Best Local Similarity: 69.23% Mismatches: 2
Query Match: 68.12% Indels: 0
DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-2533 (1-609)

OY 2 AspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
Db 440 GACAAAGCCAGACGACCTCCGCCGCAAGGATCCGCC 402

RESULT 8

US-10-437-963-3120
; Sequence 3120, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 3120
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102831C.1
US-10-437-963-3120

Alignment Scores:
Pred. No.: 12.4 Length: 792
Score: 47.00 Matches: 10
Percent Similarity: 90.91% Conservative: 0

Best Local Similarity: 90.91% Mismatches: 1
Query Match: 68.12% Indels: 0
DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-3120 (1-792)

QY 4 SerGluserThrSerAlaGlyArgAsnArgArg 14
DB 734 TCGGAGAGACACTCAGCTGGCCGCCGCCGCCGT 766

RESULT 9

US-10-437-963-63644/c

; Sequence 63644, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 63644

; LENGTH: 297

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_64867C.1

US-10-437-963-63644

Alignment Scores:

Pred. No.: 10.6 Length: 297

Score: 45.00 Matches: 9

Percent Similarity: 84.62% Conservative: 2

Best Local Similarity: 69.23% Mismatches: 2

Query Match: 65.22% Indels: 0

DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-63644 (1-297)

QY 2 AsplysSerGluserThrSerAlaGlyArgAsnArgArg 14

DB 175 GACCAAGCCGCGAGCAGACCTCCGCCGCAAGAATCGCCGC 137

RESULT 10

US-10-437-963-49610/c

; Sequence 49610, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 49610

; LENGTH: 568

; TYPE: DNA

; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52178C.1
US-10-437-963-49610

Alignment Scores:

Pred. No.: 32.8 Length: 568

Score: 44.00 Matches: 8

Percent Similarity: 84.62% Conservative: 3

Best Local Similarity: 61.54% Mismatches: 2

Query Match: 63.77% Indels: 0

DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-49610 (1-568)

QY 2 AsplysSerGluserThrSerAlaGlyArgAsnArgArg 14

DB 395 GACCAAGCCGAGCAGCAGCACCGCCGCCGCAAGAATCGCCGC 357

RESULT 11

US-10-437-963-92187/c

; Sequence 92187, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 92187

; LENGTH: 571

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_90693C.1
US-10-437-963-92187

Alignment Scores:

Pred. No.: 33 Length: 571

Score: 44.00 Matches: 8

Percent Similarity: 84.62% Conservative: 3

Best Local Similarity: 61.54% Mismatches: 2

Query Match: 63.77% Indels: 0

DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-92187 (1-571)

QY 2 AsplysSerGluserThrSerAlaGlyArgAsnArgArg 14

DB 380 GACCAAGCCAGCAGCAGCACCGCCGCCGCAAGAATCGCCGC 342

RESULT 12

US-10-437-963-64563

; Sequence 64563, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 64563
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_65695C.1
US-10-437-963-64563

Alignment Scores:
Pred. No.: 35.6 Length: 615
Score: 44.00 Matches: 8
Percent Similarity: 84.62% Conservative: 3
Best Local Similarity: 61.54% Mismatches: 2
Query Match: 63.77% Indels: 0
DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-64563 (1-615)

QY 2 ApplySerGluserThSerAlaglyArgAsnArgArg 14
Db 170 GACCAAGCCAGACGACGACGCCGCCGACGAATCGCCGC 208

RESULT 13
US-10-282-122A-26385/c
; Sequence 26385, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26385

; LENGTH: 1603
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
; US-10-282-122A-26385

Alignment Scores:
Pred. No.: 97.9 Length: 1603
Score: 44.00 Matches: 9
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 63.77% Indels: 0
DB: 16 Gaps: 0

US-09-857-841-4 (1-14) x US-10-282-122A-26385 (1-1603)

QY 3 LysSerGluserThSerAlaglyArgAsnArgArg 14
Db 1240 CGCCAGAAATCGACTTCGGCGGGCGGTGAAGA 1205

RESULT 14
US-10-282-122A-28450/c
; Sequence 28450, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28450
; LENGTH: 2625
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; US-10-282-122A-28450

Alignment Scores:
Pred. No.: 165 Length: 2625
Score: 44.00 Matches: 9
Percent Similarity: 83.33% Conservative: 1

Best Local Similarity: 75.00% Mismatches: 2
Query Match: 63.77% Indels: 0
DB: 16 Gaps: 0

US-09-857-841-4 (1-14) x US-10-282-122A-28450 (1-2625)

QY 3 LysSerGluSerThrSerAlaGlyArgAsnArgArg 14
DB 1273 CGCCGAGATCTGACTTCGCGGGGCGCGGTGGAAGA 1238

RESULT 15

US-10-437-963-86635/c

; Sequence 86635, Application US/10437963

; Publication No. US2004012343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 86635

; LENGTH: 969

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_85657C.1

US-10-437-963-86635

Alignment Scores:

Pred. No.:	89.6	Length:	969
Score:	43.00	Matches:	8
Percent Similarity:	78.57%	Conservative:	3
Best Local Similarity:	57.14%	Mismatches:	3
Query Match:	62.32%	Indels:	0
DB:	17	Gaps:	0

US-09-857-841-4 (1-14) x US-10-437-963-86635 (1-969)

QY 1 MetAspLysSerGluSerThrSerAlaGlyArgAsnArgArg 14
DB 915 ATGTCGATTTCTGACAAACACACCGCGGCGGCATCGTGA 874

Search completed: December 5, 2004, 09:47:10
Job time : 351 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 09:07:08 ; Search time 2542 Seconds
(without alignments)
260.447 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 14
Sequence: 1 MDKSESTSAGRNRR 14

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 segs, 23644849745 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9041059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool/US09857841/runat_03122004_160613_19119/app_query.fasta.1.199
-DB=GenEmbl -QFWT=fastap -SUFFIX=olip2n_rge -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc
-NORM=ext -HEAPS12E=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09857841 @CGN_1_1_3731 @runat_03122004_160613_19119 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	53	6	BD261798 Enhanceme
2	14	100.0	130	6	AR031575 Sequence
3	14	100.0	130	6	AR065687 Sequence
4	14	100.0	130	6	AR097446 Sequence

5	14	100.0	130	6	I49964	I49964 Sequence 14
6	14	100.0	131	6	AR031572	AR031572 Sequence
7	14	100.0	131	6	AR065684	AR065684 Sequence
8	14	100.0	131	6	AR097443	AR097443 Sequence
9	14	100.0	131	6	I49961	I49961 Sequence 11
10	14	100.0	152	6	AR031570	AR031570 Sequence
11	14	100.0	152	6	AR031571	AR031571 Sequence
12	14	100.0	152	6	AR065682	AR065682 Sequence
13	14	100.0	152	6	AR065683	AR065683 Sequence
14	14	100.0	152	6	AR097441	AR097441 Sequence
15	14	100.0	152	6	AR097442	AR097442 Sequence
16	14	100.0	152	6	I49959	I49959 Sequence 9
17	14	100.0	154	6	I49960	I49960 Sequence 10
18	14	100.0	154	6	AR031573	AR031573 Sequence
19	14	100.0	154	6	AR031574	AR031574 Sequence
20	14	100.0	154	6	AR065685	AR065685 Sequence
21	14	100.0	154	6	AR065686	AR065686 Sequence
22	14	100.0	154	6	AR097444	AR097444 Sequence
23	14	100.0	154	6	AR097445	AR097445 Sequence
24	14	100.0	154	6	I49962	I49962 Sequence 12
25	14	100.0	154	6	I49963	I49963 Sequence 13
26	14	100.0	654	6	E01760	E01760 DNA encodin
27	14	100.0	654	14	AF444252	AF444252 Banana mo
28	14	100.0	657	14	AB070622	AB070622 Cucumber
29	14	100.0	657	14	AB109909	AB109909 Cucumber
30	14	100.0	657	14	AF198622	AF198622 Cucumber
31	14	100.0	657	14	AF281864	AF281864 Cucumber
32	14	100.0	657	14	AF316362	AF316362 Cucumber
33	14	100.0	657	14	AF350450	AF350450 Cucumber
34	14	100.0	657	14	AF368192	AF368192 Cucumber
35	14	100.0	657	14	AF523339	AF523339 Cucumber
36	14	100.0	657	14	AF523340	AF523340 Cucumber
37	14	100.0	657	14	AF523341	AF523341 Cucumber
38	14	100.0	657	14	AF523342	AF523342 Cucumber
39	14	100.0	657	14	AF523343	AF523343 Cucumber
40	14	100.0	657	14	AF523344	AF523344 Cucumber
41	14	100.0	657	14	AF523345	AF523345 Cucumber
42	14	100.0	657	14	AF523346	AF523346 Cucumber
43	14	100.0	657	14	AF523347	AF523347 Cucumber
44	14	100.0	657	14	AF523348	AF523348 Cucumber
45	14	100.0	657	14	AF523349	AF523349 Cucumber

ALIGNMENTS

RESULT 1	BD261798	53 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD261798	Enhancement in protein production by higher plants using ubiquitin			
DEFINITION	BD261798	or cucumber mosaic virus coating protein peptide.			
ACCESSION	BD261798.1	GI:33071566			
VERSION	JP 2002532098-A/2.				
KEYWORDS	Cucumber mosaic virus				
SOURCE	Cucumber mosaic virus				
ORGANISM	Cucumovirus.				
REFERENCE	1 (bases 1 to 53)				
AUTHORS	Fang,R.X., Wu,J.L. and Chen,X.Y.				
TITLE	Enhancement in protein production by higher plants using ubiquitin				
JOURNAL	or cucumber mosaic virus coating protein peptide				
COMMENT	Patent: JP 2002532098-A 2 02-OCT-2002;				
	INSTITUTE OF MOLECULAR AGROBIOLOGY				
	OS Cucumber mosaic virus				
	PN JP 2002532098-A/2				
	PD 02-OCT-2002				
	PF 11-DEC-1998 JP 2000588378				
	PI RONG XIANG FANG,JUNG LIN WU,XIAO YING CHEN				
	PC C12N15/09,A01HS/00,C07K14/415,C07K19/00,C12N5/10,C12N15/00, PC				
	C12N5/00				
	CC Enhancement in protein production by higher plants using				
	ubiquitin or				
	CC cucumber mosaic virus coating protein peptide FH				
	Key				

Location/Qualifiers
FT CDS (6). .(47).
Location/Qualifiers
1. .53
/organism="Cucumber mosaic virus"
/mol_type="genomic DNA"
/db_xref="taxon:12305"
ORIGIN
Alignment Scores:
Pred. No.: 6.9e-06 Length: 53
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-857-841-4 (1-14) x BD261798 (1-53)
QY 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
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6 ATGGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGA 47
Db
RESULT 2
AR031575 130 bp DNA linear PAT 29-SEP-1999
LOCUS AR031575
DEFINITION Sequence 14 from patent US 5866384.
ACCESSION AR031575
VERSION AR031575.1 GI:5945864
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 130)
TITLE Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
JOURNAL Cell ablation using trans-splicing ribozymes
Patent: US 5866384-A 14 02-FEB-1999;
FEATURES location/Qualifiers
source 1. .130
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.68e-05 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-857-841-4 (1-14) x AR031575 (1-130)
QY 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
53 ATGGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGA 94
Db
RESULT 3
AR065687 130 bp DNA linear PAT 29-SEP-1999
LOCUS AR065687
DEFINITION Sequence 14 from patent US 5849548.
ACCESSION AR065687
VERSION AR065687.1 GI:5995903
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 130)
TITLE Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
JOURNAL Cell ablation using trans-splicing ribozymes
Patent: US 5849548-A 14 15-DEC-1998;
FEATURES location/Qualifiers
source 1. .130

/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.68e-05 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-857-841-4 (1-14) x AR065687 (1-130)
QY 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
53 ATGGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGA 94
Db
RESULT 4
AR097446 130 bp DNA linear PAT 14-FEB-2001
LOCUS AR097446
DEFINITION Sequence 14 from patent US 6071730.
ACCESSION AR097446
VERSION AR097446.1 GI:12806176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 130)
TITLE Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
JOURNAL Cell ablation using trans-splicing ribozymes
Patent: US 6071730-A 14 06-JUN-2000;
FEATURES location/Qualifiers
source 1. .130
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.68e-05 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-857-841-4 (1-14) x AR097446 (1-130)
QY 1 MetAspLySerGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
53 ATGGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGA 94
Db
RESULT 5
I49964 130 bp DNA linear PAT 07-OCT-1997
LOCUS I49964
DEFINITION Sequence 14 from patent US 5641673.
ACCESSION I49964
VERSION I49964.1 GI:2472184
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 130)
TITLE Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
JOURNAL Cell ablation using trans-splicing ribozymes
Patent: US 5641673-A 14 24-JUN-1997;
FEATURES location/Qualifiers
source 1. .130
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:

Pred. No.: 1.68e-05 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x I49964 (1-130)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 53 ATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGA 94

RESULT 6
AR031572

LOCUS AR031572 131 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5866384.
ACCESSION AR031572
VERSION AR031572.1 GI:5945861
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 11 02-FEB-1999;
FEATURES
source 1.131
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.69e-05 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR031572 (1-131)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 54 ATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGA 95

RESULT 7
AR065684

LOCUS AR065684 131 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5849548.
ACCESSION AR065684
VERSION AR065684.1 GI:5995900
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 11 15-DEC-1998;
FEATURES
source 1.131
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.69e-05 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR065684 (1-131)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 54 ATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGA 95

RESULT 8
AR097443

LOCUS AR097443 131 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6071730.
ACCESSION AR097443
VERSION AR097443.1 GI:12806173
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 11 06-JUN-2000;
FEATURES
source 1.131
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.69e-05 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR097443 (1-131)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 54 ATGACAAATCTGAATCAACCAAGTCTGCTGTAACCGTCGA 95

RESULT 9
I49961

LOCUS I49961 131 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 11 from patent US 5641673.
ACCESSION I49961
VERSION I49961.1 GI:2472181
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5641673-A 11 24-JUN-1997;
FEATURES
source 1.131
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.69e-05 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x I49961 (1-131)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14

Db 54 ATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGA 95

RESULT 10

AR031570

LOCUS AR031570 152 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 9 from patent US 5866384.

ACCESSION AR031570

VERSION AR031570.1 GI:5945859

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 152)

AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.

TITLE Cell ablation using trans-splicing ribozymes

JOURNAL Patent: US 5866384-A 9 02-FEB-1999;

FEATURES

source location/Qualifiers

1..152

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1.96e-05 Length: 152

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR031570 (1-152)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14

Db 75 ATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGA 116

RESULT 11

AR031571

LOCUS AR031571 152 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 10 from patent US 5866384.

ACCESSION AR031571

VERSION AR031571.1 GI:5945860

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 152)

AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.

TITLE Cell ablation using trans-splicing ribozymes

JOURNAL Patent: US 5866384-A 10 02-FEB-1999;

FEATURES

source location/Qualifiers

1..152

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/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1.96e-05 Length: 152

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR031571 (1-152)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14

Db 75 ATGATTAATCTGAATCAACCAAGTGTGCTGTAACCGTCGA 116

RESULT 12

AR065682

LOCUS AR065682 152 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 9 from patent US 5849548.

ACCESSION AR065682

VERSION AR065682.1 GI:5995898

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 152)

AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.

TITLE Cell ablation using trans-splicing ribozymes

JOURNAL Patent: US 5849548-A 9 15-DEC-1998;

FEATURES

source location/Qualifiers

1..152

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/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1.96e-05 Length: 152

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

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Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR065682 (1-152)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14

Db 75 ATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGA 116

RESULT 13

AR065683

LOCUS AR065683 152 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 10 from patent US 5849548.

ACCESSION AR065683

VERSION AR065683.1 GI:5995899

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 152)

AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.

TITLE Cell ablation using trans-splicing ribozymes

JOURNAL Patent: US 5849548-A 10 15-DEC-1998;

FEATURES

source location/Qualifiers

1..152

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1.96e-05 Length: 152

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR065683 (1-152)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14

Db 75 ATGATTAATCTGAATCAACCAAGTGTGCTGTAACCGTCGA 116

RESULT 14

AR097441

LOCUS AR097441 152 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 9 from patent US 6071730.

ACCESSION AR097441

VERSION AR097441.1 GI:12806171

KEYWORDS

LOCUS AR065682 152 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 9 from patent US 5849548.

ACCESSION AR065682

VERSION AR065682.1 GI:5995898

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 152)

AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.

TITLE Cell ablation using trans-splicing ribozymes

JOURNAL Patent: US 5849548-A 9 15-DEC-1998;

FEATURES

source location/Qualifiers

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/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1.96e-05 Length: 152

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR065682 (1-152)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14

Db 75 ATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGA 116

RESULT 13

AR065683

LOCUS AR065683 152 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 10 from patent US 5849548.

ACCESSION AR065683

VERSION AR065683.1 GI:5995899

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 152)

AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.

TITLE Cell ablation using trans-splicing ribozymes

JOURNAL Patent: US 5849548-A 10 15-DEC-1998;

FEATURES

source location/Qualifiers

1..152

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1.96e-05 Length: 152

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR065683 (1-152)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14

Db 75 ATGATTAATCTGAATCAACCAAGTGTGCTGTAACCGTCGA 116

RESULT 14

AR097441

LOCUS AR097441 152 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 9 from patent US 6071730.

ACCESSION AR097441

VERSION AR097441.1 GI:12806171

KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 9 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..152
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.96e-05 length: 152
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR097441 (1-152)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
Db 75 ATGACAAATCTGAATCAACCACTGCTGTCGTAAACCGTCGA 116

RESULT 15
AR097442 AR097442 152 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 10 from patent US 6071730.
DEFINITION AR097442
ACCESSION AR097442
VERSION AR097442.1 GI:12806172
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 10 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..152
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.96e-05 length: 152
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR097442 (1-152)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
Db 75 ATGATTAATCTGAATCAACCACTGCTGTCGTAAACCGTCGA 116

Search completed: December 5, 2004, 10:36:25
Job time : 2542 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 08:24:43 ; Search time 326 Seconds
(without alignments)
225.435 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 14
Sequence: 1 MDKSESTSAGRNR 14

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Word size: 1

Total number of hits satisfying chosen parameters: 8245260

Minimum DB seq length: 0
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseg_23Sep04:*

1:	geneseg1980s:*
2:	geneseg1990s:*
3:	geneseg2000s:*
4:	geneseg2001as:*
5:	geneseg2001bs:*
6:	geneseg2002as:*
7:	geneseg2002bs:*
8:	geneseg2003as:*
9:	geneseg2003bs:*
10:	geneseg2003cs:*
11:	geneseg2003ds:*
12:	geneseg2004s:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	53	3	AAA30858
2	14	100.0	771	2	AAT34666
3	14	100.0	772	2	AAT34664
4	14	100.0	772	2	AAT17259
5	14	100.0	773	2	AAT34665
6	14	100.0	976	2	AAQ10461

7	14	100.0	1007	2	AAQ10462	AaQ10462 Capsid pr
8	14	100.0	1007	2	AAQ67395	AaQ67395 Cauliflow
9	14	100.0	1066	2	AAT99545	Aat99545 Cucumber
10	14	100.0	1067	2	AAZ07505	Aaz07505 Cucumber
11	14	100.0	1379	1	AAAN8111	Aaan8111 Sequence
12	14	100.0	1696	2	AAQ76107	AaQ76107 Cucumber
13	14	100.0	1860	2	AAQ76106	AaQ76106 Cucumber
14	14	100.0	2173	2	AAQ76108	AaQ76108 Cucumber
15	12	85.7	657	2	AAQ03641	AaQ03641 Cucumber
16	12	85.7	894	3	ABL58209	AbL58209 Agrobacte
17	12	85.7	1423	1	AAAN90249	Aaan90249 Cucumber
18	12	85.7	1426	2	AAT72272	Aat72272 Cucumber
19	9	64.3	2208	11	ABD15071	Abd15071 Pseudomon
20	9	64.3	2361	11	ABD15266	Abd15266 Pseudomon
21	9	64.3	2862	11	ABD14864	Abd14864 Pseudomon
22	8	57.1	936	11	ABD07120	Abd07120 Pseudomon
23	8	57.1	1062	11	ABD07131	Abd07131 Pseudomon
24	8	57.1	3695	5	AAS67888	Aas67888 DNA encod
25	7	50.0	42	5	AAF25808	Aaf25808 Murine ty
26	7	50.0	51	4	AAI79772	Aai79772 Human non
27	7	50.0	215	5	ABV32121	Abv32121 Human pro
28	7	50.0	215	5	ABV41058	Abv41058 Human pro
29	7	50.0	229	3	AAC13242	Aac13242 Human sec
30	7	50.0	279	8	ABX42019	Abx42019 Bovine ES
31	7	50.0	290	5	ABV06729	Abv06729 Human pro
32	7	50.0	369	5	ABV36676	Abv36676 Human pro
33	7	50.0	369	11	ABD00834	Abd00834 Klebsiell
34	7	50.0	399	10	ABZ37724	Abz37724 N. gonorr
35	7	50.0	399	10	ABZ41931	Abz41931 N. gonorr
36	7	50.0	408	9	ACH47248	Ach47248 Human inf
37	7	50.0	428	5	ABV00831	Abv00831 Human pro
38	7	50.0	444	12	ADN73300	Adn73300 Thale cre
39	7	50.0	450	5	ABV30952	Abv30952 Human pro
40	7	50.0	452	6	ABV88244	Abv88244 Human col
41	7	50.0	456	5	ABV00609	Abv00609 Human pro
42	7	50.0	458	5	ABV31173	Abv31173 Human pro
43	7	50.0	458	5	ABV39920	Abv39920 Human pro
44	7	50.0	458	5	ABV39866	Abv39866 Human pro
45	7	50.0	458	5	ABV40142	Abv40142 Human pro

ALIGNMENTS

RESULT 1			
AAA30858	AAA30858 standard; DNA; 53 BP.		
ID	AAA30858		
XX	AAA30858;		
AC	19-SEP-2000 (first entry)		
DT	Ubiquitin monomer C-terminal fragment coding sequence.		
XX	Ubiquitin monomer; protein production; plant cell; ubiquitin promoter;		
DE	ds.		
XX	Nicotiana tabacum.		
KW			
XX			
OS			
XX			
FH	Key	Location/Qualifiers	
FT	CDS	6..47	
FT		/*tag= a	
FT		/product= "Ubiquitin_monomer_fragment"	
FT		/partial	
XX			
PN	WO200036129-A1.		
XX			
PD	22-JUN-2000.		
XX			
PF	11-DEC-1998;	98WO-SG000103.	
XX			
PR	11-DEC-1998;	98WO-SG000103.	
XX			
PA	(MOLE-) INST MOLECULAR AGROBIOLOGY.		

XX Fang R, Wu J, Chen X;
PI
XX WPI; 2000-431604/37.
DR P-PSDB; AAY90255.
XX
PT Production of desired protein in plants or plant cells by linking a
PT ubiquitin monomer coding sequence upstream of the gene encoding the
PT desired protein.
XX
PS Claim 8; Page 18; 42pp; English.
XX
XX This sequence encodes the C-terminal fragment of a ubiquitin monomer. The
CC invention relates to a method for enhancing production of a desired
CC protein in a plant or plant cell by inserting a nucleic acid (NA)
CC encoding a ubiquitin monomer upstream of a NA encoding the desired
CC protein, where the fusion construct encodes a fusion protein and
CC expression is not controlled by the ubiquitin promoter. The invention
CC also relates to a NA acid vector a NA vector able to transform a plant
CC cell, that comprises NA encoding a fusion protein having a ubiquitin
CC monomer linked to a protein of interest and further, where expression of
CC the fusion construct is not under control of a ubiquitin promoter. The
CC construct allows enhanced production of the desired protein in plants or
CC plant cells
XX
SQ Sequence 53 BP; 15 A; 14 C; 13 G; 11 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.38e-06 Length: 53
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-857-841-4 (1-14) x AAA30858 (1-53)

OY 1 MetAspIysSerGluSerThrSerAlaGlyArgAsnArgArg 14
|||
Db 6 ATGGACAAATCTGAATCAACCAAGTGTGTGTAACCGTCGA 47

RESULT 2
AAT34666
ID AAT34666 standard; DNA; 771 BP.

AC AAT34666;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)

XX Coat protein of the V34 strain of cucumber mosaic virus.

XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KW resistance; ss.

XX Cucurber mosaic virus; strain V34.

OS
XX
FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a

XX WO9621018-A1.

XX 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX

DR WPI; 1996-333993/33.
DR P-PSDB; AAR98895.
XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
PS Claim 24; Fig 3; 80pp; English.

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX
SQ Sequence 771 BP; 176 A; 199 C; 183 G; 213 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.67e-05 Length: 771
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAT34666 (1-771)

OY 1 MetAspIysSerGluSerThrSerAlaGlyArgAsnArgArg 14
|||
Db 3 ATGGACAAATCTGAATCAACCAAGTGTGTGTAACCGTCGA 44

RESULT 3
AAT34664
ID AAT34664 standard; DNA; 772 BP.

AC AAT34664;

XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)

XX Coat protein of the V27 strain of cucumber mosaic virus.

XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KW resistance; ss.

XX Cucurber mosaic virus; strain V27.

OS
XX
FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a

XX WO9621018-A1.

XX 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX

XX WPI; 1996-333993/33.

XX P-PSDB; AAR98893.

PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.

PS Claim 2; Fig 1; 80pp; English.

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 772 BP; 177 A; 202 C; 182 G; 211 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.68e-05 Length: 772
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAT34664 (1-772)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
ATAT17259
ID AAT17259 standard; DNA; 772 BP.
XX AC AAT17259;
XX DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX OS Coat protein of the A35 strain of cucumber mosaic virus.
DE
XX KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance; ss.
XX OS Cucumber mosaic virus; strain A35.
XX FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a

XX PN WO9621018-A1.

XX PD 11-JUL-1996.

XX PF 07-JUN-1995; 95WO-US007234.

XX PR 30-DEC-1994; 94US-00367789.

XX PA (ASGR-) ASGROW SEED CO.

XX PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

XX PS WPI; 1996-333993/33.

XX DR P-PSDB; AAR93803.

XX PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.

XX PS Disclosure; Fig 8; 80pp; English.

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 772 BP; 175 A; 201 C; 185 G; 211 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.68e-05 Length: 772
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAT17259 (1-772)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
ATG34665
ID AAT34665 standard; DNA; 773 BP.
XX AC AAT34665;
XX DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX OS Coat protein of the V33 strain of cucumber mosaic virus.
DE
XX KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance; ss.
XX OS Cucumber mosaic virus; strain V33.
XX FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a

XX PN WO9621018-A1.

XX PD 11-JUL-1996.

XX PF 07-JUN-1995; 95WO-US007234.

XX PR 30-DEC-1994; 94US-00367789.

XX PA (ASGR-) ASGROW SEED CO.

XX PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

XX PS WPI; 1996-333993/33.

XX DR P-PSDB; AAR98894.

XX PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.

XX PS Claim 13; Fig 2; 80pp; English.

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 773 BP; 175 A; 200 C; 185 G; 213 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.68e-05 Length: 773
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAT34665 (1-773)

AAQ67395
ID AAQ67395 standard; DNA; 1007 BP.
XX
AC AAQ67395;
XX
DT 25-MAR-2003 (revised)
DT 12-APR-1995 (first entry)
XX
DE Cauliflower mosaic virus capsid protein coding sequence.
XX
KM Cauliflower mosaic virus; CMV; capsid protein; coat protein;
KW polyribozyme; inactivate; inactivation; resistance; crop protection; ss.
XX
OS Cauliflower mosaic virus.
XX
FH Key Location/Qualifiers
FT CDS 54..710
FT /*tag= a
FT /product= "Capsid protein."
XX
PN FR2701960-A1.
XX
PD 02-SEP-1994.
XX
PF 26-FEB-1993; 93FR-00002269.
XX
PR 26-FEB-1993; 93FR-00002269.
XX
PA (GENE-) GENE SHEARS PTY LTD.
XX
PI Lenée P, Perez P, Gruber V, Baudot G, Ollivo C;
XX
DR WPI; 1994-281767/35.
DR P-PSDB; AAR57968.
XX
PT New polyribozyme contg. several catalytic regions in complementary
PT sequence - can inactivate gene for viral capsid protein, esp. for prepn.
PT of new virus resistant transgenic plants, also DNA sequence encoding it.
XX
PS Disclosure; Fig 2; 67pp; French.
XX
CC The RNA encoding the capsid protein of cauliflower mosaic virus can be
CC targeted by a nucleic acid sequence called a "polyribozyme". The
CC polyribozyme has endoribonuclease activity and is able to inactivate the
CC gene encoding the viral capsid protein. The polyribozyme comprises
CC several catalytic regions derived from ribozymes and confers complete
CC resistance to virus. See AAQ67391-94. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 5.91e-05 Length: 1007
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
XX
US-09-857-841-4 (1-14) x AAQ67395 (1-1007)
QY 1 MetAspIysSerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 54 ATGACAAATCTGAATCAACGAGTGTGTCGTAACCGTCGA 95
XX
RESULT 9
ID AAT99545/c
XX AAT99545 standard; cDNA; 1066 BP.
AC AAT99545;
XX
DT 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)

XX
DE Cucurber mosaic virus RNA-3 cDNA fragment.
XX
KM Transgenic plant; virus resistance; disease resistance; RNA virus; CMV;
KW coat protein; antisense gene; ss.
XX
OS Cucurber mosaic virus.
XX
FH Key Location/Qualifiers
FT 3'UTR 1..299
FT /*tag= a
FT CDS 300..958
FT /*tag= b
FT /product= "coat protein"
FT sig_peptide 956..1029
FT /*tag= c
FT /note= "coat protein leader sequence"
FT promoter 1030..1066
FT /*tag= d
FT /note= "F sequence of sub-genomic promoter"
XX
PN EP806481-A2.
XX
PD 12-NOV-1997.
XX
PF 07-MAY-1997; 97EP-00201379.
XX
PR 09-MAY-1996; 96IT-MI000927.
XX
PA (META-) METAPONTUM AGROBIOS SCRL.
XX
PI Cellini F, Grieco PD;
XX
DR WPI; 1997-538620/50.
XX
PT Preparing transgenic plants resistant to RNA virus infection - using
PT anti:sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
PS Claim 3; Page 10; 18pp; English.
XX
CC This cDNA clone of cucumber mosaic virus (CMV) RNA-3 includes domain F of
CC the subgenomic promoter of viral RNA, the coat protein gene, its leader
CC sequence, and the tRNA-like 3'-terminal region of RNA-3. It was prepared
CC by amplifying a fragment of CMV cDNA-3 from clone PCR-CMV1RNA3 by PCR
CC (see also AAT99548-49). The gene construct is introduced into a vector
CC containing a promoter active in plant cells in antisense orientation
CC relative to the promoter. A claimed recombinant vector comprises the
CC plant promoter, the antisense gene construct and a terminator which is
CC functional in the plant. In addition to CMV, viral RNA may also be used
CC from tobacco mosaic virus and potato virus. Claimed transgenic plants
CC have the antisense gene construct integrated into their genomes. They are
CC resistant to viral infection. In particular, they are resistant to CMV.
CC Within the antisense gene construct, the interfering activity of the
CC antisense F domain of the sub-genomic promoter, associated with the
CC antisense activity performed by the coat protein gene, allows production
CC of plants having 100% resistance to CMV. (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 1066 BP; 299 A; 251 C; 273 G; 243 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 6.22e-05 Length: 1066
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
XX
US-09-857-841-4 (1-14) x AAT99545 (1-1066)
QY 1 MetAspIysSerGluSerThrSerAlaGlyArgAsnArgArg 14
XX

Db 956 ATGACAAATCTGAATCAACCAAGTCTGTCGTACCGTCGA 915

RESULT 10
AAZ07505/c
ID AAZ07505 standard; cDNA; 1067 BP.
XX
AC AAZ07505;
XX
DT 26-NOV-1999 (first entry)
XX
DE Cucumber mosaic virus (CMV) RNA-3 gene cDNA clone fragment.
XX
KW Transgenic plant; RNA virus; antisense construct; cucumber mosaic virus;
CMV; promoter; coat protein gene; infection; RNA-3; ss.
XX
OS Cucumber mosaic virus.
XX
PN US5959181-A.
XX
PD 28-SEP-1999.
XX
PF 09-MAY-1997; 97US-00854170.
XX
PR 09-MAY-1996; 96IT-MI000927.
XX
PA (META-) METAPONTUM AGROBIOS SCRL.
XX
PI Cellini F, Grieco PD;
XX
DR WPI; 1997-538620/50.
XX
PT Preparing transgenic plants resistant to RNA virus infection - using
PT anti:sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
XX Claim 2; Fig 1; 15pp; English.

CC The invention relates to preparing transgenic plants resistant to RNA
CC virus induced infections that comprises integrating an antisense gene
CC construct into the plant genome. The construct comprises: (a) an F domain
CC of a subgenomic promoter of cucumber mosaic virus (CMV); (b) downstream
CC from the subgenomic promoter, a leader sequence of a coat protein gene of
CC CMV; (c) downstream from the leader sequence, a gene encoding a CMV coat
CC protein; and (d) downstream from the gene, a 3'-terminal region of a CMV
CC coat protein gene. The method is useful for producing plants which are
CC resistant to infection by RNA based viruses. The gene construct gives
CC higher levels of resistance compared to antisense constructs which are
CC capable of complementing with different domains of genomic RNA of CMV.
CC The present sequence represents the fragment of cDNA clone of RNA-3 of
CC CMV. This forms the antisense construct of the invention
XX
SQ Sequence 1067 BP; 297 A; 250 C; 276 G; 244 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.22e-05 Length: 1067
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAZ07505 (1-1067)

QY 1 MetAplysSerGluSerThrSeraIaGlyARgAsnARgArg 14
ID AAN81111 standard; DNA; 1379 BP.
XX
AC AAN81111;
XX

Db 956 ATGACAAATCTGAATCAACCAAGTCTGTCGTACCGTCGA 915

RESULT 11
AAN81111
ID AAN81111 standard; DNA; 1379 BP.
XX
AC AAN81111;
XX

DT 25-MAR-2003 (revised)
DT 12-NOV-1990 (first entry)
XX
DE Sequence contg. CMV strain Y coat protein gene.
XX
KW Cucumber mosaic virus; plant viral resistance; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 418..1074
FT /*tag= a
FT /label= cucumber mosaic virus-Y coat protein.
XX
PN EP279433-A.
XX
PD 24-AUG-1988.
XX
PF 18-FEB-1988; 88EP-00102322.
XX
PR 20-FEB-1987; 87JP-00038288.
PR 25-FEB-1987; 87JP-00043443.
PR 18-FEB-1988; 88JP-00035809.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Furusawa I, Onda H, Komiya T;
XX
DR WPI; 1988-236708/34.
DR P-PSDB; AAP80509.
XX
PT DNA coding for the coat protein of cucumber mosaic virus strain Y - used
PT for producing plants resistant to cucumber mosaic virus infection.
XX
XX Disclosure; Page ?; 20pp; English.

CC This DNA is produced on screening of a plasmid library and is used to
CC transform plant cells which subsequently produce the coat prot- ein of
CC cucumber mosaic virus (CMV) strain Y. This protein is not synthesised in
CC natural plant cells. The resistance to CMV infect- ion, provided by the
CC DNA, is shown in plant cells and redifferent- iated plant bodies. See
CC also AAN81110. (Updated on 25-MAR-2003 to correct PR field.) (Updated on
CC 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1379 BP; 306 A; 342 C; 333 G; 398 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.81e-05 Length: 1379
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-857-841-4 (1-14) x AAN81111 (1-1379)

QY 1 MetAplysSerGluSerThrSeraIaGlyARgAsnARgArg 14
ID AAN81111 standard; DNA; 1696 BP.
XX
AC AAN81111;
XX

Db 418 ATGACAAATCTGAATCAACCAAGTCTGTCGTACCGTCGA 459

RESULT 12
AAQ76107
ID AAQ76107 standard; DNA; 1696 BP.
XX
AC AAQ76107;
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE Cucumber mosaic virus RNA-3 chimera encoding RNase T1.
XX
KW Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
virus resistance; disease resistance; transgenic plant; cross protection;

KW hypersensitive response; crop improvement; tomato;
KM Lycopersicon esculentum; tobacco; Nicotiana tabacum; RNase T1;
KW cell inhibitory protein; ToMV; CMV; ss.
XX Cucumber mosaic virus.
OS
FH Key Location/Qualifiers
FT CDS 123..437
FT /*tag= a
FT /product= "RNase T1"
XX
PN WO9429464-A1.
XX
PD 22-DEC-1994.
XX
PF 03-JUN-1994; 94WO-EP001817.
XX
PR 04-JUN-1993; 93GB-00011593.
XX
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI De Haan PT;
XX
XX WPI; 1995-036490/05.
DR P-PSDB; AAR67754.
PT
PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.
XX
PS Claim 4, Page 31-32; 50pp; English.
XX
CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76107) has the coat
CC protein gene replaced by a gene encoding a cell inhibitory protein, RNase
CC T1, having the sequence given in AAR67754. The construct elicits a minus-
CC sense RNA that interacts with the RNA-dependent RNA-polymerase of an
CC invading virus, thus conferring virus-resistance on a host plant, e.g.
CC tobacco, tomato. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 1696 BP; 387 A; 413 C; 389 G; 507 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.38e-05 Length: 1696
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ76107 (1-1696)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
DB 733 ATGGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 774

RESULT 13
AAQ76106
ID AAQ76106 standard; DNA; 1860 BP.
XX
XX AAQ76106;
AC
XX 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE Cucumber mosaic virus RNA-3 chimera encoding ToMV CP.
XX
KW Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; coat protein; CP;
KM ToMV; CMV; ss.

XX
OS Cucumber mosaic virus.
XX
FH Key Location/Qualifiers
FT CDS 123..600
FT /*tag= a
FT /product= "ToMV coat protein"
FT CDS 895..1550
FT /*tag= b
FT /product= "CMV coat protein"
XX
PN WO9429464-A1.
XX
PD 22-DEC-1994.
XX
PF 03-JUN-1994; 94WO-EP001817.
XX
PR 04-JUN-1993; 93GB-00011593.
XX
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI De Haan PT;
XX
XX WPI; 1995-036490/05.
DR P-PSDB; AAR67752, AAR67753.
PT
PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.
XX
PS Claim 3, Page 27-28; 50pp; English.
XX
CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76106) codes for the
CC coat protein (CP) of tomato mosaic virus (AAR67752) as well as its own CP
CC (AAR67753). The construct elicits minus-sense RNA that interacts with the
CC RNA-dependent RNA-polymerase of an invading virus, thus conferring virus-
CC resistance on a host plant, e.g. tobacco, tomato. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 1860 BP; 448 A; 429 C; 431 G; 552 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000102 Length: 1860
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ76106 (1-1860)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
DB 897 ATGGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 938

RESULT 14
AAQ76108
ID AAQ76108 standard; DNA; 2173 BP.
XX
XX AAQ76108;
AC
XX 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE Cucumber mosaic virus RNA-3 chimera encoding ToMV P30.
XX
KW Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; P30; elicitor; ToMV;
KM CMV; ss.

XX OS Cucumber mosaic virus.
XX XX
FH Key Location/Qualifiers
FT CDS 123..914
FT /*tag=a
FT /product="Tomv P30 elicitor"
XX
PN WO9429464-A1.
XX
XX PD 22-DEC-1994.
XX
XX PF 03-JUN-1994; 94WO-EP001817.
XX PR 04-JUN-1993; 93GB-00011593.
XX
XX (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI De Haan PT;
XX
XX WPI; 1995-036490/05.
DR P-PSDB; AAR67755.
XX
XX
PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.
XX
XX PS Claim 5; Page 34-35; 50pp; English.
XX
XX A chimeric cucumber mosaic virus RNA-3 (given in AAQ76108) has the coat
CC protein gene replaced by a gene encoding an elicitor, Tomv P30, having
CC the sequence given in AAR67755. The construct elicits a minus-sense RNA
CC that interacts with the RNA-dependent RNA-polymerase of an invading
CC virus, thus conferring virus-resistance on a host plant, e.g. tobacco,
CC tomato. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 2173 BP; 561 A; 438 C; 532 G; 642 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000117 Length: 2173
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ76108 (1-2173)

QY 1 MetAaPlySserGluSerThrSerAlaGlyArgAsnArgarg 14
Db 1210 ATGGACAAATCTGAATCAACCAAGTGCTGCTGTAACCGTGA 1251

RESULT 15
AAQ03641
ID AAQ03641 standard; DNA; 657 BP.
XX
XX AAQ03641;
XX
XX 24-OCT-2003 (revised)
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 07-AUG-1990 (first entry)
XX
XX Cucumber Mosaic Virus-C (CMV-C) coat protein gene.
XX
XX CMV-C; curcubitaceae; solanaceae; ds.
XX
XX Cucumber mosaic virus; strain C.
XX
XX WO9002185-A.

PD 08-MAR-1990.
XX
XX PF 02-AUG-1989; 89WO-US003288.
XX
XX PR 19-AUG-1988; 88US-00234404.
XX
XX PA (UPJO) UPJOHN CO.
XX (CORR) CORNELL RES FOUND INC.
XX
XX PI Quemada H, Slightom JL, Gonsalves D, Kearney C;
XX
XX WPI; 1990-099409/13.
DR
XX
XX PT Coat protein gene of cucumber mosaic virus strain WL - cloned to produce
PT transformed plants which are resistant to CMV viral infection.
XX
XX PS Disclosure; Page ?; 18pp; English.
XX
XX CC The sequence encodes the coat protein of CMV-C. (Updated on 25-MAR-2003
CC to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 27-AUG-2003 to correct OS field.) (Updated on 24-OCT-2003 to
CC standardise OS field)
XX
XX SQ Sequence 657 BP; 157 A; 176 C; 151 G; 173 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00396 Length: 657
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.71% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ03641 (1-657)

QY 1 MetAaPlySserGluSerThrSerAlaGlyArgAsn 12
Db 1 ATGGACAAATCTGAATCAACCAAGTGCTGCTGTAAC 36

Search completed: December 5, 2004, 09:53:57
Job time : 328 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 09:41:23 ; Search time 2043 Seconds
(without alignments)
249.709 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 14
Sequence: 1 MDKSESTSAGRNR 14

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 segs, 18219865908 residues

Word size: 1

Total number of hits satisfying chosen parameters: 65640016

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09857841/runat_03122004_160613_19127/app_query.fasta_1.199
-DB=BST_QFMT=fastap -SUFFIX=olip2n.rst -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09857841@CGN_1_1_3437@runat_03122004_160613_19127 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_htc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	14	100.0	127	4	BM067231	BM067231 KS08001E1
C 2	9	64.3	801	8	BZ560224	BZ560224 pac62-164
C 3	8	64.3	957	8	BZ571483	BZ571483 msh2_191.
C 4	8	57.1	172	2	BB574268	BB574268 BB574268
C 5	8	57.1	297	2	AW390465	AW390465 RC3-ST018
C 6	8	57.1	402	1	AA560203	AA560203 v120h03.r
C 7	8	57.1	536	8	AO612674	AO612674 HS_5107_B
C 8	8	57.1	589	9	CE588296	CE588296 tigr-gss-
C 9	8	57.1	594	7	CF568862	CF568862 FAMU_USDA

C 10	8	57.1	679	8	AZ419370	AZ419370 IM0195P18
C 11	8	57.1	686	8	AZ964281	AZ964281 2M0233J19
C 12	8	57.1	816	8	AZ741218	AZ741218 RPCI-24-1
C 13	8	57.1	823	4	BI851822	BI851822 603378972
C 14	8	57.1	839	8	BZ603235	BZ603235 WHADA95TF
C 15	8	57.1	889	9	CG137878	CG137878 PUCIG49TD
C 16	8	57.1	899	9	CG225585	CG225585 OGVHE83TV
C 17	8	57.1	900	9	CC623795	CC623795 OGVBO38TH
C 18	8	57.1	908	9	CC623807	CC623807 OGVBO38TV
C 19	8	57.1	939	2	BE895594	BE895594 601438392
C 20	8	57.1	953	5	BU112365	BU112365 603130810
C 21	8	57.1	964	9	CG368624	CG368624 OG2BF09TV
C 22	8	57.1	1015	5	BU147745	BU147745 AGENCOURT
C 23	8	57.1	1345	8	CC312068	CC312068 TAM32-15K
C 24	8	57.1	1678	8	CC222612	CC222612 CH261-183
C 25	8	57.1	1907	2	BF144190	BF144190 601788894
C 26	7	50.0	109	1	AA784543	AA784543 e9e07a1.f
C 27	7	50.0	118	6	CD945181	CD945181 RDV_22_Ge
C 28	7	50.0	118	6	CD960094	CD960094 SDA_136_G
C 29	7	50.0	129	8	CC387216	CC387216 PUIHW90TB
C 30	7	50.0	136	8	BH804848	BH804848 1008105D0
C 31	7	50.0	145	6	CF096437	CF096437 QHN23C23.
C 32	7	50.0	148	8	AZ481650	AZ481650 IM0306I03
C 33	7	50.0	156	7	CO744011	CO744011 TGESTzyo9
C 34	7	50.0	162	9	CG541742	CG541742 OST135287
C 35	7	50.0	177	2	AW859218	AW859218 MRI-CT035
C 36	7	50.0	193	2	AW859260	AW859260 MRI-CT035
C 37	7	50.0	201	8	CC114971	CC114971 NDL.47119
C 38	7	50.0	207	1	AV264210	AV264210 AV264210
C 39	7	50.0	215	9	CG481915	CG481915 OST14620
C 40	7	50.0	219	9	CG483642	CG483642 OST17351
C 41	7	50.0	224	2	AW210914	AW210914 uc089c04.Y
C 42	7	50.0	234	1	AI212359	AI212359 x3f08a1.f
C 43	7	50.0	234	9	CG490292	CG490292 OST27407
C 44	7	50.0	235	9	CG632317	CG632317 OST350317
C 45	7	50.0	240	7	F25547	F25547 HSPD12640 H

ALIGNMENTS

RESULT 1
BM067231/c
LOCUS BM067231 127 bp mRNA linear EST 11-SEP-2002
DEFINITION KS08001E12 KS08 Capsicum annuum cDNA, mRNA sequence.
ACCESSION BM067231
VERSION BM067231.1 GI:22787366
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Capsicum.

REFERENCE 1 (bases 1 to 127)
Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S.,
Hur,C.-G. and Choi,D.

TITLE Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
annuum L.) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen

JOURNAL COMMENT

Unpublished (2001)
Contact: Doil Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309

FEATURES
source
Email: doil@mail.krrib.re.kr
High quality sequence stop: 127.
Location/Qualifiers

1..127
/organism="Capsicum annuum"
/mol_type="mRNA"
/cultivar="Hang Keun"
/db_xref="taxon:4072"

ORIGIN /tissue_type="anther"
/dev_stage="10 weeks after germination"
/clone_lib="KS08"
/note="Vector: pBluescript SK(-)"

Alignment Scores:
Pred. No.: 7.61e-05 Length: 127
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-857-841-4 (1-14) x BM067231 (1-127)

QY 1 MetAplysSerGlUSeRThSerAlaGlyARgAsnARgArg 14
|||||
Db 78 ATGGACAAATCTGAATCAACCACTGCTGTCGTAACCGTCGA 37

RESULT 2
BZ560224/c BZ560224 801 bp DNA linear GSS 17-DEC-2002
LOCUS pacs2-164_2261.xl pacs2-164 Pseudomonas aeruginosa genomic clone
DEFINITION pacs2-164_2261, genomic survey sequence.
ACCESSION BZ560224
VERSION BZ560224.1 GI:27177889
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 801)
AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library

JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
Genome Center

University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

FEATURES
source location/Qualifiers
1..801
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
/clone_lib="pacs2-164_2261"
/clone_lib="pacs2-164"
/note="Clinical isolate 2-164 whole genomic shotgun
library."

ORIGIN
Alignment Scores:
Pred. No.: 37 Length: 801
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.29% Indels: 0
DB: 8 Gaps: 0

US-09-857-841-4 (1-14) x BZ560224 (1-801)

QY 6 SerThrSerAlaGlyARgAsnARgArg 14
|||||
Db 458 AGTACATCGCGCGGTAGAAACCGCGCT 432

RESULT 3

BZ571483/c BZ571483 957 bp DNA linear GSS 17-DEC-2002
LOCUS msh2_191.y1 msh Pseudomonas aeruginosa genomic clone msh2_191,
genomic survey sequence.

ACCESSION BZ571483
VERSION BZ571483.1 GI:27206544
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 957)
AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library

JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

FEATURES
source location/Qualifiers
1..957
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="MSH"
/db_xref="taxon:287"
/clone_lib="msh2_191"
/clone_lib="msh"
/note="Environmental isolate. Whole genomic shotgun
library."

ORIGIN

Alignment Scores:
Pred. No.: 43.5 Length: 957
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.29% Indels: 0
DB: 8 Gaps: 0

US-09-857-841-4 (1-14) x BZ571483 (1-957)

QY 6 SerThrSerAlaGlyARgAsnARgArg 14
|||||
Db 422 AGTACATCGCGCGGTAGAAACCGCGCT 396

RESULT 4
BB574268 BB574268 172 bp mRNA linear EST 30-NOV-2000
LOCUS BB574268 RIKEN full-length enriched, 11 days pregnant adult female
DEFINITION ovary and uterus Mus musculus cDNA clone 5033401A11, mRNA sequence.
ACCESSION BB574268
VERSION BB574268.1 GI:11470812
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 172)
AUTHORS Alizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T.,
Carninci,P., Hanagaki,T., Hayatsu,N., Hirooka,T., Hirozane,T.,
Hodoyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J.,
Kojima,Y., Konno,H., Kusakabe,M., Matsuyama,T., Miyazaki,A.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Okazaki,Y.,
Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K.,
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,T., Toya,T.,
Matahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A.,

TITLE
JOURNAL
COMMENT

Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22. Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.

FEATURES
Source

Location/Qualifiers
1..172
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5033401A11"
/sex="female"
/tissue_type="ovary and uterus"
/dev_stage="11 days pregnant, adult"
/lab_host="DH10B"
/clone_1ib="RIKEN full-length enriched, 11 days pregnant
adult female ovary and uterus"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTVN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATTCGAGTTAATTAAATTAATCCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified Bluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
BamHI."

ORIGIN

Alignment Scores:
Pred. No.: 88.8 Length: 172
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x BB574268 (1-172)

Qy 7 ThrSerAlaGlyArgAsnArgArg 14
|||||
Db 16 ACCTCCGCTGTCCGAATCCCGG 39

RESULT 5
AW390465 297 bp mRNA linear EST 04-FEB-2000
LOCUS
DEFINITION
RC3-ST0186-181099-012-c02 ST0186 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AW390465
VERSION
AW390465.1 GI:6895124
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS
HCGP http://www.ludwig.org.br/ORESTES.
TITLE
The FAPESP/LICR Human Cancer Genome Project
JOURNAL
Unpublished (1999)
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimposon@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC3&t2=RC3-ST0186-
181099-012-c02&t3=1999-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 40
High quality sequence stop: 128.
Location/Qualifiers
1..297

FEATURES
Source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1ib="ST0186"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 146 Length: 297
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AW390465 (1-297)

Qy 7 ThrSerAlaGlyArgAsnArgArg 14
|||||
Db 130 ACCAGCGCAGAGAGACAGAAGG 153

RESULT 6
AA560203 402 bp mRNA linear EST 18-AUG-1997
LOCUS
DEFINITION
v120h03.r1 StrataGene mouse Tcell 937311 Mus musculus cDNA clone
IMAGE:972821 5', mRNA sequence.
ACCESSION
AA560203
VERSION
AA560203.1 GI:2331668
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 402)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Scheilenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:553549 Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 387. Location/Qualifiers

FEATURES

source 1..402 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGE:972821" /cissue_type="Tcell" /dev_stage="M30 CD4+ cells" /lab_host="SOLR (kanamycin resistant)" /clone_lib="Stratagene mouse Tcell 937311" /note="Organ: blood; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGACGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTT TTT TTT TTT TTT TTT 3'"

ORIGIN

Alignment Scores:

Pred. No.:	193	Length:	402
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	57.14%	Indels:	0
DB:	1	Gaps:	0

US-09-857-841-4 (1-14) x AA560203 (1-402)

Qy 7 ThrsEra1aG1yArGAsnArGArG 14

LOCUS |||||||||||||||||||

DEFINITION HS 5107 B2 E12 T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=683 Col=24 Row=J, genomic survey sequence.

ACCESSION AQ612674

VERSION AQ612674.1 GI:5073950

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 536) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE 99380589

PUBMED 10449764

COMMENT Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end web server: <http://www.htsc.washington.edu>

Plate: 683 row: J column: 24

Seq primer: T7

Class: BAC ends

High quality sequence stop: 536. Location/Qualifiers

FEATURES

source 1..536 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="Plate=683 Col=24 Row=J" /sex="male" /clone_lib="RPCI-11 Human Male BAC Library" /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

ORIGIN

Alignment Scores:

Pred. No.:	251	Length:	536
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	57.14%	Indels:	0
DB:	8	Gaps:	0

US-09-857-841-4 (1-14) x AQ612674 (1-536)

Qy 5 GluSerThrsEra1aG1yArGAsn 12

LOCUS |||||||||||||||||||

DEFINITION tigr-gss-dog-17000366361600 Dog Library Canis familiaris genomic, genomic survey sequence.

ACCESSION CE588296

VERSION CE588296.1 GI:36905077

KEYWORDS GSS.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

AUTHORS 1 (bases 1 to 589) Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.

TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)

MEDLINE 22875432

PUBMED 14512627

COMMENT Contact: Kirkness EF The Institute for Genomic Research Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-0200 Fax: 301-838-0208 Email: ekirknes@tigr.org Class: shotgun. Location/Qualifiers

FEATURES

source 1..589
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Alignment Scores:
Pred. No.: 273 length: 589
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 9 Gaps: 0

US-09-857-841-4 (1-14) x CFS68862 (1-589)

Qy 5 GluSerThrSerAlaGlyArgAsn 12
|||||
Db 516 GAGTCAACCACTGCTGGAAGAAC 493

RESULT 9
CFS68862 594 bp mRNA linear EST 23-SEP-2003
LOCUS FAMU USDA FP 00084 Vitis shuttleworthii L., grape Vitis
DEFINITION shuttleworthii cDNA 5', mRNA sequence.
ACCESSION CFS68862
VERSION CFS68862.1 GI:34994945
KEYWORDS EST.
SOURCE Vitis shuttleworthii
ORGANISM Vitis shuttleworthii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 594)
Hunter,W.B., Dang,P.M., Chaparro,J.X., Lu,J. and Leong,S.
Genes expressed in Vitis shuttleworthii L
Unpublished (2004)
Contact: Jiang Lu, FAMU, Wayne Hunter, USDA,ARS
Viticulture Centre, FAMU, Tallahassee, FL
Florida A&M University
Tallahassee, FL 32317, USA
Tel: (850) 412-7393
Fax: (850) 561-2617, (772) 462-5898
Email: jiang.lu@fam.u.edu,
Seq primer: T3 Primer.
Location/Qualifiers
1..594
/organism="Vitis shuttleworthii"
/mol_type="mRNA"
/db_xref="taxon:246827"
/sex="Mixed population"
/tissue_type="Fruit tendril, leaves, bud, flowers"
/dev_stage="At blooming"
/lab_host="XLI-Blue"
/clone_lib="Vitis shuttleworthii L., grape"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; A high quality EST with at least 100 contiguous
bases at Trace Tuner score of 20 or better. Construction
by PM Dang, USDA, ARS, U.S. Horticultural Research Lab,
Ft. Pierce, FL, USA."

ORIGIN

Alignment Scores:
Pred. No.: 275 length: 594
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 7 Gaps: 0

US-09-857-841-4 (1-14) x CFS68862 (1-594)

Qy 7 ThrSerAlaGlyArgAsnArg 14
|||||
Db 82 ACATCTGCAGGAGAAATCGAGA 105

RESULT 10
AZ419370/c 679 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0195P18R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0195P18 R, genomic survey sequence.
ACCESSION AZ419370
VERSION AZ419370.1 GI:10543383
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 679)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0195 row: P column: 18
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 679.
Location/Qualifiers
1..679
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0195P18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Alignment Scores:
Pred. No.: 311 length: 679

Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 8 Gaps: 0

US-09-857-841-4 (1-14) x AZ419370 (1-679)

QY 7 ThrSerAlaGlyArgAsnArg 14
Db 63 ACCTCTGCAGCAGGAATCGTAGA 40

RESULT 11

AZ964281/c 686 bp DNA linear GSS 27-APR-2001
LOCUS 2M0233J19R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0233J19 R, genomic survey sequence.

ACCESSION AZ964281 GI:13835508
VERSION AZ964281
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 686)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: J column: 19
Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 686.

FEATURES
source

1. 686
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0233J19"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

ORIGIN and selected for ampicillin resistance."

Alignment Scores: 314 Length: 686
Pred. No.: 8.00 Matches: 8
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 57.14% Gaps: 0
DB: 8

US-09-857-841-4 (1-14) x AZ964281 (1-686)

QY 6 SerThrSerAlaGlyArgAsnArg 13
Db 163 TCTACATCAGCAGGAATATAGA 140

RESULT 12
AZ741218/c 816 bp DNA linear GSS 25-JAN-2001
LOCUS RPCI-24-145M10.TJ RPCI-24 Mus musculus genomic clone
DEFINITION RPCI-24-145M10, genomic survey sequence.

ACCESSION AZ741218 GI:12515463
VERSION AZ741218
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 816)
Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSs: RPCI-24-145M10.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 145 row: M column: 10
Seq primer: SP6
Class: BAC ends.

FEATURES
source

1. 816
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-145M10"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."

ORIGIN

Alignment Scores: 368 Length: 816
Pred. No.: 8.00 Matches: 8
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00%

Query Match: 57.14% Indels: 0
DB: 8 Gaps: 0

US-09-857-841-4 (1-14) x AZ741218 (1-816)

Qy 3 LysSerGluSerThrSerAlaGly 10
Db 487 AAGTCAGAGTCTACTTCTGCTGGT 464

RESULT 13
BI851822/c 823 bp mRNA linear EST 10-OCT-2001
LOCUS 603378972F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5391617 5',
DEFINITION mRNA sequence.
ACCESSION BI851822
VERSION BI851822
KEYWORDS BI851822.1 GI:15992569
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 823)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM11997 row: p column: 18
High quality sequence stop: 773.
Location/Qualifiers
1. .823
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5391617"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN

Alignment Scores:

Pred. No.:	371	Length:	823
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	57.14%	Indels:	0
DB:	4	Gaps:	0

US-09-857-841-4 (1-14) x BI851822 (1-823)

Qy 5 GluSerThrSerAlaGlyArgAsn 12
Db 727 GAGAGCACACGCGCTGAGAAAT 704

RESULT 14
BZ603235 839 bp DNA linear GSS 08-JUN-2003
LOCUS BZ603235
DEFINITION WHADA95TF Human MCF7 breast cancer cell line library (MCF7_1) Homo
sapiens genomic clone MCF7_1-19021, genomic survey sequence.
ACCESSION BZ603235

VERSION BZ603235.1 GI:31511697
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 839)
Volik,S., Zhao,S., Chin,K., Brebner,J.H., Herndon,D.R., Tao,Q.,
Kowbel,D., Huang,G., Lapuk,A., Kuo,W.-L., Magrane,G., de Jong,P.,
Gray,J.W. and Collins,C.
End-sequence profiling: Sequence-based analysis of aberrant genomes
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
22709111
12788976
PUBMED
TITLE Contact: Volik SV
JOURNAL Colin Collins' lab
MEDLINE UCSF Comprehensive Cancer Center
PUBMED UCSF Box 0808, San Francisco, CA 94143-0808, USA
12788976
Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
Class: BAC ends.

FEATURES
source
1. .839
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="MCF7_1-19021"
/sex="female"
/clone_lib="Human MCF7 breast cancer cell line library
(MCF7_1)"
/note="Vector: pECBAC1; Site_1: HindIII; This library was
constructed from MCF7 breast cancer cell line by Amplicon
Express (http://www.genomex.com) using their standard
procedure."

ORIGIN

Alignment Scores:

Pred. No.:	378	Length:	839
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	57.14%	Indels:	0
DB:	8	Gaps:	0

US-09-857-841-4 (1-14) x BZ603235 (1-839)

Qy 4 SerGluSerThrSerAlaGlyArg 11
Db 721 TCAGAAAGCACCTCAGCAGTCGG 744

RESULT 15
CG137878/c 889 bp DNA linear GSS 21-AUG-2003
LOCUS CG137878
DEFINITION PUICG49TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBtra0550J01,
genomic survey sequence.
ACCESSION CG137878
VERSION CG137878.1 GI:34028661
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 889)
Whitelew,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUICG49TB

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 09:47:13 ; Search time 68 Seconds
(without alignments)
146.339 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 14
Sequence: 1 MDKSESTSGRNRR 14

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Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 segs, 355394441 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1640630

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
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6: /cgn2_6/ptodata/1/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	14	100.0	130	2	US-08-488-031-14 Sequence 14, Appl
3	14	100.0	130	2	US-08-486-569-14 Sequence 14, Appl
4	14	100.0	130	2	US-08-488-027-14 Sequence 14, Appl
5	14	100.0	130	2	US-08-090-192-14 Sequence 14, Appl
6	14	100.0	130	2	US-08-482-663-14 Sequence 14, Appl
7	14	100.0	130	3	US-08-482-658-14 Sequence 14, Appl
8	14	100.0	130	3	US-08-470-349-14 Sequence 14, Appl
9	14	100.0	130	3	US-08-475-610-14 Sequence 14, Appl
10	14	100.0	130	5	PCT-US92-00277-14 Sequence 14, Appl
11	14	100.0	130	5	PCT-US92-00278-14 Sequence 14, Appl
12	14	100.0	131	1	US-08-090-193-11 Sequence 11, Appl

13	14	100.0	131	2	US-08-488-031-11	Sequence 11, Appl
14	14	100.0	131	2	US-08-486-569-11	Sequence 11, Appl
15	14	100.0	131	2	US-08-488-027-11	Sequence 11, Appl
16	14	100.0	131	2	US-08-090-192-11	Sequence 11, Appl
17	14	100.0	131	2	US-08-482-663-11	Sequence 11, Appl
18	14	100.0	131	3	US-08-482-658-11	Sequence 11, Appl
19	14	100.0	131	3	US-08-470-349-11	Sequence 11, Appl
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24	14	100.0	152	1	US-08-090-193-10	Sequence 9, Appl
25	14	100.0	152	2	US-08-488-031-9	Sequence 9, Appl
26	14	100.0	152	2	US-08-488-031-10	Sequence 9, Appl
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32	14	100.0	152	2	US-08-090-192-10	Sequence 10, Appl
33	14	100.0	152	2	US-08-482-663-9	Sequence 9, Appl
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44	14	100.0	153	5	PCT-US92-00278-12	Sequence 12, Appl
45	14	100.0	154	1	US-08-090-193-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-090-193-14
Sequence 14, Application US/08090193
Patent No. 5641673
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andreea
APPLICANT: Perrimon, No. 5641673bert
TITLE OF INVENTION: Goodmann, Howard M.
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,193
FILING DATE: 23-DEC-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimballa, Michele A.
REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0609.3080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-090-193-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-857-841-4 (1-14) x US-08-090-193-14 (1-130)

QY 1 MetaspYsSerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 53 ATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGA 94

RESULT 2
US-08-488-031-14
Sequence 14, Application US/08488031
Patent No. 5849548
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5849548bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,031
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080002/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both

TOPOLOGY: linear
US-08-488-031-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-031-14 (1-130)

QY 1 MetaspYsSerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 53 ATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGA 94

RESULT 3
US-08-486-569-14
Sequence 14, Application US/08486569
Patent No. 5863774
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5863774bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,569
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080006/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-486-569-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-569-14 (1-130)

QY 1 MetAaplySergIuserThrSeraIagIYArgAsnArg 14
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Db 53 ATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTGA 94

RESULT 4

US-08-488-027-14

; Sequence 14, Application US/08488027

; Patent No. 5866384

; GENERAL INFORMATION:

; APPLICANT: Haseloff, James

; APPLICANT: Brand, Andrea

; APPLICANT: Perrimon, No. 5866384bert

; APPLICANT: Goodman, Howard M.

; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, N.W., Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488, 027

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/090,193

; FILING DATE: 23-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00277

; FILING DATE: 16-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/642,330

; FILING DATE: 17-JAN-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Bugalsky, Lawrence B.

; REGISTRATION NUMBER: 35,086

; REFERENCE/DOCKET NUMBER: 0609.3080003/MAC/LBB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 130 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; US-08-488-027-14

Alignment Scores:

Pred. No.:	3.32e-06	Length:	130
Score:	14.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-857-841-4 (1-14) x US-08-488-027-14 (1-130)

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Db 53 ATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTGA 94

RESULT 5

US-08-090-192-14

; Sequence 14, Application US/08090192

; Patent No. 5874414

; GENERAL INFORMATION:

; APPLICANT: Haseloff, James

; APPLICANT: Goodman, Howard M.

; TITLE OF INVENTION: Trans-Splicing Ribozymes

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/090,192

; FILING DATE: 11-NOV-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/ US 92/00278

; FILING DATE: 16-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/642,333

; FILING DATE: 17-JAN-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Cimbala, Michele A.

; REGISTRATION NUMBER: 33,851

; REFERENCE/DOCKET NUMBER: 0609.3030001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 130 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: both

; US-08-090-192-14

Alignment Scores:

Pred. No.:	3.32e-06	Length:	130
Score:	14.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-857-841-4 (1-14) x US-08-090-192-14 (1-130)

QY 1 MetAaplySergIuserThrSeraIagIYArgAsnArg 14
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Db 53 ATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTGA 94

RESULT 6

US-08-482-663-14

; Sequence 14, Application US/08482663

; Patent No. 5882907

; GENERAL INFORMATION:

; APPLICANT: Haseloff, James

; APPLICANT: Brand, Andrea

; APPLICANT: Perrimon, No. 5882907bert

; APPLICANT: Goodman, Howard M.

; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, N.W., Suite 600

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; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/090,193
; FILING DATE: 23-DEC-1993
; APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3080005/MAC/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
;
US-08-482-663-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-482-663-14 (1-130)

QY 1 MetAsplysSerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 53 ATGACAAATCTGATCAACCACTGCTGCTGTAACCGTCGA 94

RESULT 7
US-08-482-658-14
; Sequence 14, Application US/08482658
; Patent No. 6010904
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perrimon, No. 6010904bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,658
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/090,193
; FILING DATE: 23-DEC-1993
; APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3080008/MAC/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
;
US-08-482-658-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-857-841-4 (1-14) x US-08-482-658-14 (1-130)

QY 1 MetAsplysSerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 53 ATGACAAATCTGATCAACCACTGCTGCTGTAACCGTCGA 94

RESULT 8
US-08-470-349-14
; Sequence 14, Application US/08470349
; Patent No. 6015794
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,349
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/090,192
; FILING DATE: 11-NOV-1993
; APPLICATION NUMBER: PCT/ US 92/00278
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,333
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FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-470-349-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-857-841-4 (1-14) x US-08-470-349-14 (1-130)

QY 1 MetAplysSergUserThrsEraLaGlyArgAsnArgArg 14
DB 53 ATGACAAATCTGAATCAACCAAGTGTGTCGTACCGTCGA 94

RESULT 9
US-08-475-610-14
Sequence 14, Application US/08475610
Patent No. 6071730
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 6071730bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,610
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080004/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-475-610-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-857-841-4 (1-14) x US-08-475-610-14 (1-130)

QY 1 MetAplysSergUserThrsEraLaGlyArgAsnArgArg 14
DB 53 ATGACAAATCTGAATCAACCAAGTGTGTCGTACCGTCGA 94

RESULT 10
PCT-US92-00277-14
Sequence 14, Application PC/TUS9200277
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, Norbert
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 19920116
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3496604
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 833-7533
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US92-00277-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-857-841-4 (1-14) x PCT-US92-00277-14 (1-130)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 53 ATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 94

RESULT 11

PCT-US92-00278-14
; Sequence 14, Application PC/TUS9200278
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Avenue, N.W., Suite 300
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00278
; FILING DATE: 19920116
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,333
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.3476604
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)833-7533
; TELEFAX: (202)833-8716
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Nucleic Acid
; PCT-US92-00278-14

Alignment Scores:

Pred. No.:	3.32e-06	Length:	130
Score:	14.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

US-09-857-841-4 (1-14) x PCT-US92-00278-14 (1-130)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 53 ATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 94

RESULT 12

US-08-090-193-11
; Sequence 11, Application US/08090193
; Patent No. 5641673
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perrimon, No. 5641673bert
; APPLICANT: Goodman, Howard M.

; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090,193
; FILING DATE: 23-DEC-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0609.3080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-090-193-11

Alignment Scores:

Pred. No.:	3.34e-06	Length:	131
Score:	14.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-857-841-4 (1-14) x US-08-090-193-11 (1-131)

QY 1 MetAspLySserGluSerThrSerAlaGlyArgAsnArgArg 14
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Db 54 ATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 95

RESULT 13

US-08-488-031-11
; Sequence 11, Application US/08488031
; Patent No. 5849548
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perrimon, No. 5849548bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,031
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080002/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-488-031-11

Alignment Scores:
Pred. No.: 3.34e-06 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-031-11 (1-131)

QY 1 MetAspIySserGluSerThrSerAlaGlyArgAsnArgArg 14
Db 54 ATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 95

RESULT 14

US-08-486-569-11
Sequence 11, Application US/08486569
Patent No. 5863774
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5863774bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,569
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080006/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-486-569-11

Alignment Scores:
Pred. No.: 3.34e-06 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-486-569-11 (1-131)

QY 1 MetAspIySserGluSerThrSerAlaGlyArgAsnArgArg 14
Db 54 ATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGA 95

RESULT 15

US-08-488-027-11
Sequence 11, Application US/08488027
Patent No. 5866384
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5866384bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,027
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086

REFERENCE/DOCKET NUMBER: 0609.3080003/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-488-027-11

Alignment Scores:
Pred. No.: 3.34e-06 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-027-11 (1-131)

QY 1 MetAspLysSerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 54 ATGGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGA 95

Search completed: December 5, 2004, 11:11:50
Job time : 68 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 09:48:28 ; Search time 351 Seconds
(without alignments)
219.166 Million cell updates/sec

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Perfect score: 14
Sequence: 1 MDKSESTSGRNRR 14

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Ygapop 60.0 , Ygapext 60.0
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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14	100.0	771	13	US-10-011-033-5	Sequence 5, Appli
2	14	100.0	772	13	US-10-011-033-1	Sequence 1, Appli
3	14	100.0	772	13	US-10-011-033-14	Sequence 14, Appl
4	14	100.0	792	13	US-10-011-033-3	Sequence 3, Appli
5	12	85.7	960	13	US-10-011-033-9	Sequence 9, Appli
6	8	57.1	792	17	US-10-437-963-3120	Sequence 3120, Ap
7	7	50.0	107	16	US-10-424-599-140904	Sequence 140904,
8	7	50.0	166	18	US-10-425-115-66023	Sequence 66023, A
9	7	50.0	233	16	US-10-424-599-94618	Sequence 94618, A
10	7	50.0	279	9	US-09-960-352-7184	Sequence 7184, Ap
11	7	50.0	316	18	US-10-425-115-46484	Sequence 46484, A
12	7	50.0	408	10	US-09-918-995-34460	Sequence 34460, A
13	7	50.0	452	9	US-09-998-598-1555	Sequence 1555, Ap
14	7	50.0	464	9	US-09-864-761-15219	Sequence 15219, A
15	7	50.0	478	18	US-10-425-115-174482	Sequence 174482,
16	7	50.0	509	13	US-10-027-632-234457	Sequence 234457,
17	7	50.0	509	15	US-10-027-632-234457	Sequence 234457,
18	7	50.0	518	15	US-10-029-386-11750	Sequence 11750, A
19	7	50.0	563	16	US-10-424-599-31741	Sequence 31741, A
20	7	50.0	570	15	US-10-424-599-11368	Sequence 11368, A
21	7	50.0	627	18	US-10-425-115-59660	Sequence 59660, A
22	7	50.0	654	15	US-10-156-761-7305	Sequence 7305, Ap
23	7	50.0	715	18	US-10-425-115-42949	Sequence 42949, A
24	7	50.0	726	15	US-10-156-761-4748	Sequence 4748, Ap
25	7	50.0	747	18	US-10-425-115-61926	Sequence 61926, A
26	7	50.0	819	15	US-10-369-493-37738	Sequence 37738, A
27	7	50.0	852	16	US-10-424-599-42689	Sequence 42689, A
28	7	50.0	855	15	US-10-126-103-37	Sequence 37, Appl
29	7	50.0	855	16	US-10-431-096-37	Sequence 37, Appl
30	7	50.0	902	16	US-10-424-599-110979	Sequence 110979,
31	7	50.0	956	16	US-10-425-114-13912	Sequence 13912, A
32	7	50.0	1071	14	US-10-198-846-10820	Sequence 10820, A
33	7	50.0	1138	10	US-09-822-846-464	Sequence 464, App
34	7	50.0	1323	15	US-10-369-493-32000	Sequence 32000, A
35	7	50.0	1347	17	US-10-437-963-67382	Sequence 67382, A
36	7	50.0	1467	15	US-10-156-761-6326	Sequence 6326, Ap
37	7	50.0	1471	9	US-09-764-869-455	Sequence 455, App
38	7	50.0	1471	14	US-10-091-504-455	Sequence 455, App
39	7	50.0	1471	16	US-10-227-577-455	Sequence 455, App
40	7	50.0	1554	15	US-10-369-493-35770	Sequence 35770, A
41	7	50.0	1566	15	US-10-369-493-44194	Sequence 44194, A
42	7	50.0	1603	16	US-10-343-710-78	Sequence 78, Appl
43	7	50.0	1603	16	US-10-282-122A-26385	Sequence 26385, A
44	7	50.0	1635	16	US-10-282-122A-7523	Sequence 7523, Ap
45	7	50.0	1657	18	US-10-425-115-138705	Sequence 138705,

ALIGNMENTS

RESULT 1
US-10-011-033-5
; Sequence 5, Application US/10011033
; Publication No. US20020124286A1

GENERAL INFORMATION:

APPLICANT: McShore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois

COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber mosaic virus
STRAIN: V-34
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
OTHER INFORMATION: /codon start= 3
/function= "ENCAPSIDATES VIRUS RNA"
/product= "COAT PROTEIN"
/gene= "CP"
/number= 1
/standard name= "COAT PROTEIN"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-011-033-5
Alignment Scores:
Pred. No.: 9.49e-06 Length: 771
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-5 (1-771)
QY 1 MetAspLySergLuserThrSerAlaGlyArgAsnArgArg 14
Db 3 ATGACAAATCTGAATCAACCAAGTCTGTGCTGAACCGTCGA 44
RESULT 2
US-10-011-033-1
Sequence 1, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: V-27
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-011-033-1
Alignment Scores:
Pred. No.: 9.5e-06 Length: 772
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-1 (1-772)
QY 1 MetAspLySergLuserThrSerAlaGlyArgAsnArgArg 14
Db 3 ATGACAAATCTGAATCAACCAAGTCTGTGCTGAACCGTCGG 44
RESULT 3
US-10-011-033-14
Sequence 14, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: A35
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-011-033-14
Alignment Scores:
Pred. No.: 9.5e-06 Length: 772
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-14 (1-772)
QY 1 MetAspLySergLuserThrSerAlaGlyArgAsnArg 14
Db 3 ATGACAAATCTGAATCAACCAAGTCTGTCGTAAACCGTCGA 44
RESULT 4
US-10-011-033-3
Sequence 3, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: v-33
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-011-033-3
Alignment Scores:
Pred. No.: 9.7e-06 Length: 792
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-3 (1-792)
QY 1 MetAspLySergLuserThrSerAlaGlyArgAsnArg 14
Db 3 ATGACAAATCTGAATCAACCAAGTCTGTCGTAAACCGTCGA 44
RESULT 5
US-10-011-033-9
Sequence 9, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: STRAIN C
FEATURE:
NAME/KEY: CDS
LOCATION: 1..658
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-011-033-9

Alignment Scores:
Pred. No.: 0.00135 Length: 960
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.71% Indels: 0
DB: 13 Gaps: 0

US-09-857-841-4 (1-14) x US-10-011-033-9 (1-960)

OY 1 MetAplysSerGluserThrSerAlaGlyArgAsn 12
Db 1 ATGACCAAACTGTAATCAACCACTGCTGCTGTAAC 36

RESULT 6
US-10-437-963-3120
Sequence 3120, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 3120
LENGTH: 792
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_102831C.1
US-10-437-963-3120

Alignment Scores:
Pred. No.: 16.4 Length: 792
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-3120 (1-792)

OY 4 SerGluserThrSerAlaGlyArg 11
Db 734 TCGAGAGCACCTCAGCTGGCCGC 757

RESULT 7
US-10-424-599-140904
Sequence 140904, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 140904
LENGTH: 107
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_98246C.1
US-10-424-599-140904

Alignment Scores:
Pred. No.: 35.2 Length: 107
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 16 Gaps: 0

US-09-857-841-4 (1-14) x US-10-424-599-140904 (1-107)

OY 3 LysSerGluserThrSerAla 9
Db 54 AAATCAGATCGACTTCTGCT 74

RESULT 8
US-10-425-115-66023
Sequence 66023, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 66023
LENGTH: 166
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(166)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_160212C.1
US-10-425-115-66023

Alignment Scores:
Pred. No.: 50.3 Length: 166
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 18 Gaps: 0

US-09-857-841-4 (1-14) x US-10-425-115-66023 (1-166)

QY 8 SerAlaGlyArgAsnArgArg 14
Db 56 AGTGGCGGAGAGAAATAGAGAG 76

RESULT 9

US-10-424-599-94618

; Sequence 94618, Application US/10424599
; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223) B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 94618

; LENGTH: 233

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_56451C.1

US-10-424-599-94618

Alignment Scores:
Pred. No.: 66.3 Length: 233
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 16 Gaps: 0

US-09-857-841-4 (1-14) x US-10-424-599-94618 (1-233)

QY 7 ThrSerAlaGlyArgAsnArg 13
Db 85 ACCAGCGCCGGAGAAACAGA 105

RESULT 10

US-09-960-352-7184

; Sequence 7184, Application US/09960352

; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Tao, Nengbing

; APPLICANT: Byatt, John C.

; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

; FILE REFERENCE: 16511.006/37-21(10298) C

; CURRENT APPLICATION NUMBER: US/09/960,352

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 7184

; LENGTH: 279

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 31-LIB3057-014-Q1-K1-H3

US-09-960-352-7184

Alignment Scores:
Pred. No.: 76.8 Length: 279
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 9 Gaps: 0

US-09-857-841-4 (1-14) x US-09-960-352-7184 (1-279)

QY 7 ThrSerAlaGlyArgAsnArg 13
Db 131 ACATCAGCAGACGACGACCGT 151

RESULT 11

US-10-425-115-46484

; Sequence 46484, Application US/10425115
; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222) B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 46484

; LENGTH: 316

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_142399C.1

US-10-425-115-46484

Alignment Scores:
Pred. No.: 85 Length: 316
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 18 Gaps: 0

US-09-857-841-4 (1-14) x US-10-425-115-46484 (1-316)

QY 3 LysSerGluSerThrSerAla 9
Db 161 AAAGCGAGCAGCAGCTCAGCC 181

RESULT 12

US-09-918-995-34460

; Sequence 34460, Application US/09918995

; Publication No. US20030073623A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; PRIOR FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 34460

; LENGTH: 408

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-918-995-34460

Alignment Scores:
Pred. No.: 105 Length: 408
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 50.00% Indels: 0
DB: 10 Gaps: 0

US-09-857-841-4 (1-14) x US-09-918-995-34460 (1-408)

QY 8 SerAlaGlyArgAsnArgArg 14
DB 143 TCGGCTGGAAGAAATCGAGG 163

RESULT 13

US-09-998-598-1555/c
; Sequence 1555, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 1555
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-1555

Alignment Scores:

Pred. No.: 114 Length: 452
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 9 Gaps: 0

US-09-857-841-4 (1-14) x US-09-998-598-1555 (1-452)

QY 5 GluSerThrSerAlaGlyArg 11
DB 87 GAGTCGACGTCAGCGGAGG 67

RESULT 14

US-09-864-761-15219
; Sequence 15219, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 15219
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011288.1
US-09-864-761-15219

Alignment Scores:
Pred. No.: 116 Length: 464
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 9 Gaps: 0

US-09-857-841-4 (1-14) x US-09-864-761-15219 (1-464)

QY 4 SerGluSerThrSerAlaGly 10
DB 38 TCAGAAAGCACTCAGCTGCT 58

RESULT 15

US-10-425-115-174482/c
; Sequence 174482, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 174482
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_90708C.1
US-10-425-115-174482

Alignment Scores:
Pred. No.: 119 Length: 478
Score: 7.00 Matches: 7

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	50.00%	Indels:	0
DB:	18	Gaps:	0

US-09-857-841-4 (1-14) x US-10-425-115-174482 (1-478)

QY	4	SerGluserThrSerAlaGly	10
DB	243	TCGAAAGCACGTCGGCAGGT	223

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Job time : 353 secs

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OM protein - protein search, using sw model

Run on: December 5, 2004, 08:14:04 ; Search time 66 Seconds
(without alignments)
75.647 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 14
Sequence: 1 MDKSESTSGRNRR 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1582122 seqs, 356623098 residues

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Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

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Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	218	13	US-10-011-033-2 Sequence 2, Appli
2	14	100.0	218	13	US-10-011-033-4 Sequence 6, Appli
3	14	100.0	218	13	US-10-011-033-6 Sequence 4, Appli
4	14	100.0	218	13	US-10-011-033-15 Sequence 15, Appli
5	12	85.7	218	13	US-10-011-033-10 Sequence 10, Appli
6	7	50.0	35	15	US-10-424-599-283746 Sequence 283746,
7	7	50.0	183	15	US-10-425-114-51049 Sequence 51049, A
8	7	50.0	343	15	US-10-425-114-53499 Sequence 53499, A
9	7	50.0	375	17	US-10-425-115-323368 Sequence 323368,
10	7	50.0	448	16	US-10-437-963-169865 Sequence 169865,
11	7	50.0	469	15	US-10-424-599-236497 Sequence 236497,
12	6	42.9	15	16	US-10-203-915A-131 Sequence 131, App
13	6	42.9	15	16	US-10-203-915A-132 Sequence 132, App

14	6	42.9	15	16	US-10-203-915A-133 Sequence 133, App
15	6	42.9	54	15	US-10-424-599-145411 Sequence 145411,
16	6	42.9	65	17	US-10-425-115-311170 Sequence 311170,
17	6	42.9	68	17	US-10-425-115-288412 Sequence 288412,
18	6	42.9	78	15	US-10-424-599-256382 Sequence 256382,
19	6	42.9	81	17	US-10-425-115-352829 Sequence 352829,
20	6	42.9	83	15	US-10-424-599-145321 Sequence 145321,
21	6	42.9	83	17	US-10-425-115-311232 Sequence 311232,
22	6	42.9	85	17	US-10-425-115-205605 Sequence 205605,
23	6	42.9	91	17	US-10-425-115-244053 Sequence 244053,
24	6	42.9	98	17	US-10-425-115-356957 Sequence 356957,
25	6	42.9	100	16	US-10-437-963-103201 Sequence 103201,
26	6	42.9	105	16	US-10-437-963-177629 Sequence 177629,
27	6	42.9	107	17	US-10-425-115-291239 Sequence 291239,
28	6	42.9	126	15	US-10-425-114-59079 Sequence 59079, A
29	6	42.9	127	16	US-10-437-963-124842 Sequence 124842,
30	6	42.9	131	16	US-10-437-963-105655 Sequence 105655,
31	6	42.9	135	15	US-10-425-114-58305 Sequence 58305, A
32	6	42.9	142	16	US-10-437-963-110739 Sequence 110739,
33	6	42.9	156	16	US-10-437-963-121791 Sequence 121791,
34	6	42.9	160	17	US-10-425-115-261076 Sequence 261076,
35	6	42.9	168	15	US-10-425-114-39432 Sequence 39432, A
36	6	42.9	171	17	US-10-425-115-330960 Sequence 330960,
37	6	42.9	176	17	US-10-425-115-284516 Sequence 284516,
38	6	42.9	199	16	US-10-437-963-196177 Sequence 196177,
39	6	42.9	202	16	US-10-437-963-110737 Sequence 110737,
40	6	42.9	223	14	US-10-369-493-19842 Sequence 19842, A
41	6	42.9	240	15	US-10-282-122A-70451 Sequence 70451, A
42	6	42.9	250	17	US-10-425-115-235635 Sequence 235635,
43	6	42.9	251	15	US-10-425-114-39110 Sequence 39110, A
44	6	42.9	263	16	US-10-408-765A-2608 Sequence 2608, Ap
45	6	42.9	272	17	US-10-425-115-287096 Sequence 287096,

ALIGNMENTS

RESULT 1
US-10-011-033-2
; Sequence 2, Application US/10011033
; Publication No. US20020124286A1
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; McMaster, J. Russell
; Tricoli, David M
; Reynolds, John F
; Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; Cucumber Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,033
; FILING DATE: 13-NO. US20020124286A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-011-033-2

Query Match 100.0%; Score 14; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 2
US-10-011-033-4
; Sequence 4, Application US/10011033
; Publication No. US20020124286A1
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; McMaster, J. Russell
; Tricoli, David M
; Reynolds, John F
; Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; Cucumber Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,033
; FILING DATE: 13-No. US20020124286A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-011-033-4

Query Match 100.0%; Score 14; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 3
US-10-011-033-6
; Sequence 6, Application US/10011033
; Publication No. US20020124286A1
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; McMaster, J. Russell
; Tricoli, David M
; Reynolds, John F
; Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; Cucumber Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,033
; FILING DATE: 13-No. US20020124286A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-011-033-6

Query Match 100.0%; Score 14; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 4
US-10-011-033-15
; Sequence 15, Application US/10011033
; Publication No. US20020124286A1
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; McMaster, J. Russell
; Tricoli, David M
; Reynolds, John F
; Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; Cucumber Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago

STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-011-033-15

Query Match 100.0%; Score 14; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
DB 1 MDKSESTSAGRNR 14

RESULT 5
US-10-011-033-10
Sequence 10, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L.
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-011-033-10

Query Match 85.7%; Score 12; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 12
DB 1 MDKSESTSAGRNR 12

RESULT 6
US-10-424-599-283746
Sequence 283746, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 283746
LENGTH: 35
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_98246C.1.pep
US-10-424-599-283746

Query Match 50.0%; Score 7; DB 15; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KSESTSA 9
DB 18 KSESTSA 24

RESULT 7
US-10-425-114-51049
Sequence 51049, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 51049
LENGTH: 183
TYPE: PRT
ORGANISM: Zea mays

FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-062-F2_FLI.pep
US-10-425-114-51049

Query Match 50.0%; Score 7; DB 15; Length 183;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ESTSAGR 11
| | | | |
Db 84 ESTSAGR 90

RESULT 8

US-10-425-114-53499
; Sequence 53499, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 53499
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700836661_FLI.pep
US-10-425-114-53499

Query Match 50.0%; Score 7; DB 15; Length 343;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KSESTSA 9
| | | | |
Db 28 KSESTSA 34

RESULT 9

US-10-425-115-323368
; Sequence 323368, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 323368
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_57983C.1.pep
US-10-425-115-323368

Query Match 50.0%; Score 7; DB 17; Length 375;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ESTSAGR 11
| | | | |
Db 276 ESTSAGR 282

RESULT 10

US-10-437-963-169865
; Sequence 169865, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169865
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(448)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68245C.1.pep
US-10-437-963-169865

Query Match 50.0%; Score 7; DB 16; Length 448;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ESTSAGR 11
| | | | |
Db 307 ESTSAGR 313

RESULT 11

US-10-424-599-236497
; Sequence 236497, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 236497
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_55584C.1.pep
US-10-424-599-236497

Query Match 50.0%; Score 7; DB 15; Length 469;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KSESTSA 9
|||||
DB 28 KSESTSA 34

RESULT 12
US-10-203-915A-131

; Sequence 131, Application US/10203915A
; Publication No. US20040106159A1
; GENERAL INFORMATION:
; APPLICANT: Kern, Florian
; TITLE OF INVENTION: Method for Antigen-Specific Stimulation of T
; FILE REFERENCE: 010266wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/203, 915A
; CURRENT FILING DATE: 2002-08-15
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 131
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HCMV pp65
; OTHER INFORMATION: Fragment
US-10-203-915A-131

Query Match 42.9%; Score 6; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 STSAGR 11
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DB 10 STSAGR 15

RESULT 13

US-10-203-915A-132

; Sequence 132, Application US/10203915A
; Publication No. US20040106159A1
; GENERAL INFORMATION:
; APPLICANT: Kern, Florian
; TITLE OF INVENTION: Method for Antigen-Specific Stimulation of T
; FILE REFERENCE: 010266wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/203, 915A
; CURRENT FILING DATE: 2002-08-15
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 132
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HCMV pp65
; OTHER INFORMATION: Fragment
US-10-203-915A-132

Query Match 42.9%; Score 6; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 STSAGR 11
|||||
DB 6 STSAGR 11

RESULT 14

US-10-203-915A-133

; Sequence 133, Application US/10203915A
; Publication No. US20040106159A1
; GENERAL INFORMATION:
; APPLICANT: Kern, Florian

; TITLE OF INVENTION: Method for Antigen-Specific Stimulation of T
; FILE REFERENCE: 010266wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/203, 915A
; CURRENT FILING DATE: 2002-08-15
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 133
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HCMV pp65
; OTHER INFORMATION: Fragment
US-10-203-915A-133

Query Match 42.9%; Score 6; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 STSAGR 11
|||||
DB 2 STSAGR 7

RESULT 15

US-10-424-599-145411

; Sequence 145411, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 145411
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102325C.1.pep
US-10-424-599-145411

Query Match 42.9%; Score 6; DB 15; Length 54;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSES 6
|||||
DB 1 MDKSES 6

Search completed: December 5, 2004, 08:19:00
Job time : 67 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2004, 08:05:52 ; Search time 92 Seconds
(without alignments)
87.557 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 14
Sequence: 1 MDKSESTSAGRNR 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	217	2 Q6T7D4	Q6t7d4 cucumber mo
2	14	100.0	217	2 Q66133	Q66133 cucumber mo
3	14	100.0	217	2 Q8QTRA0	Q8qta0 banana mosa
4	14	100.0	217	2 AAR89478	Aar89478 cucumber
5	14	100.0	218	1 COAT_CMVAS	Q66154 cucumber mo
6	14	100.0	218	1 COAT_CMVBA	Q66135 cucumber mo
7	14	100.0	218	1 COAT_CMVC7	Q40983 cucumber mo
8	14	100.0	218	1 COAT_CMVCS	Q66143 cucumber mo
9	14	100.0	218	1 COAT_CMVEC	Q00259 cucumber mo
10	14	100.0	218	1 COAT_CMVFT	Q66140 cucumber mo
11	14	100.0	218	1 COAT_CMV11	P14767 cucumber mo
12	14	100.0	218	1 COAT_CMV11	Q83271 cucumber mo
13	14	100.0	218	1 COAT_CMV11	Q83269 cucumber mo
14	14	100.0	218	1 COAT_CMV11	Q00260 cucumber mo
15	14	100.0	218	1 COAT_CMV11	Q66138 cucumber mo
16	14	100.0	218	1 COAT_CMVNT	Q40980 cucumber mo
17	14	100.0	218	1 COAT_CMVNT	P16489 cucumber mo
18	14	100.0	218	1 COAT_CMVNT	Q00261 cucumber mo
19	14	100.0	218	1 COAT_CMVNT	P18027 cucumber mo
20	14	100.0	218	1 COAT_CMVNT	Q89125 cucumber mo
21	14	100.0	218	2 O90712	O90712 cucumber mo
22	14	100.0	218	2 Q6Q4B0	Q6q4b0 cucumber mo
23	14	100.0	218	2 Q6Q4B0	Q6qhd0 cucumber mo
24	14	100.0	218	2 Q6S519	Q6ssi9 cucumber mo
25	14	100.0	218	2 Q6T7E2	Q6t7e2 cucumber mo
26	14	100.0	218	2 Q6U1J9	Q6ulj9 cucumber mo
27	14	100.0	218	2 Q6U1R4	Q6ulr4 cucumber mo
28	14	100.0	218	2 Q6U1R5	Q6ulr5 cucumber mo
29	14	100.0	218	2 Q6U6T0	Q6u6t0 cucumber mo
30	14	100.0	218	2 Q6U718	Q6u718 cucumber mo
31	14	100.0	218	2 Q6UB07	Q6ub07 cucumber mo

32	14	100.0	218	2 Q76U37	Q76u37 cucumber mo
33	14	100.0	218	2 Q7TDD9	Q7tda9 cucumber mo
34	14	100.0	218	2 Q7TDV0	Q7tdv0 cucumber mo
35	14	100.0	218	2 Q7THU8	Q7thu8 cucumber mo
36	14	100.0	218	2 Q66131	Q66131 cucumber mo
37	14	100.0	218	2 Q66132	Q66132 cucumber mo
38	14	100.0	218	2 Q66155	Q66155 cucumber mo
39	14	100.0	218	2 Q66157	Q66157 cucumber mo
40	14	100.0	218	2 Q83257	Q83257 cucumber mo
41	14	100.0	218	2 Q83258	Q83258 cucumber mo
42	14	100.0	218	2 Q83259	Q83259 cucumber mo
43	14	100.0	218	2 Q83260	Q83260 cucumber mo
44	14	100.0	218	2 Q8JJK5	Q8jkk5 cucumber mo
45	14	100.0	218	2 Q8JNX8	Q8jnx8 cucumber mo

ALIGNMENTS

RESULT 1
ID Q6T7D4 PRELIMINARY; PRT; 217 AA.
AC Q6T7D4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, last annotation update)
DE Coat protein.
OS Cucumber mosaic virus (cucumber mosaic cucumovirus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=12305;
RN [1]
RP SEQUENCE FROM N.A.
RA Yan L., Xu Z., Goldbach R., Chen K., Prine M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY429437; AAR89478.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 217 AA; 24015 MW; 32D0035B4F20E891 CRC64;

Query Match 100.0%; Score 14; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 2
ID Q66133 PRELIMINARY; PRT; 217 AA.
AC Q66133;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Coat protein.
OS Cucumber mosaic virus (cucumber mosaic cucumovirus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=12305;
RN [1]
RP SEQUENCE FROM N.A.
RA Reichel H., Marino L., Kummert J., Belalcazar S., Narvaez J.;
RT "Caracterizaci3n del gen de la prote3na de la caps3de de dos
RT aislamientos del virus del mosaico del pepino (CMV), obtenidos de
RT platano y banana (Musa spp.).";

RL Revista Corpoica 1:1-5(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Marino-Ramirez L.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U32859; AAB50176.1; -.
DR PIR; JC6073; JC6073.
DR PIR; JC6075; JC6075.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 217 AA; 24015 MW; 7251B7E67192DCAB CRC64;

Query Match 100.0%; Score 14; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 3
Q8QTA0 PRELIMINARY; PRT; 217 AA.
AC Q8QTA0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Coat protein.
OS Banana mosaic virus.
OC Viruses; unclassified viruses.
OX NCBI_TaxID=179820;
RN [1]
RP SEQUENCE FROM N.A.
RA Daolin D., Jie S., Peng Z., Zhixin L., Xiaodong D., Xueqing Z.;
RT "Cloning and Reconstruction of a Expression Vector for the Banana
RT Mosaic Virus Coat Protein Gene."
RL Guangxi Zhi Wu 0:0-0(2002).
DR EMBL; AF444252; AAL48223.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 217 AA; 23739 MW; 3873A80567D3B3AE CRC64;

Query Match 100.0%; Score 14; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 4
AAR89478 PRELIMINARY; PRT; 217 AA.
ID AAR89478;
AC AAR89478;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Coat protein.
OS Cucumber mosaic virus (cucumber mosaic cucumovirus).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=12305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS;
RA Yan L., Xu Z., Goldbach R., Chen K., Prins M.;
RT "Complete nucleotide sequence of cucumber mosaic virus (CS isolate)
RT RNA3."
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY429437; AAR89478.1; -.
KW Coat protein.
SQ SEQUENCE 217 AA; 24015 MW; 32D0035B4F20E891 CRC64;

Query Match 100.0%; Score 14; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 5
COAT_CMVAS STANDARD; PRT; 218 AA.
ID COAT_CMVAS
AC Q66154;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumber mosaic virus (strain As) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117118;
RN [1]
RP SEQUENCE FROM N.A.
RA Hyon S., Park Y.I.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.
CC -----
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CC -----
CC EMBL; X77855; CAA54846.1; -.
DR PIR; S42098; S42098.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24044 MW; E6BEC2E3D4CD73EF CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 6
COAT_CMVBA STANDARD; PRT; 218 AA.
ID COAT_CMVBA
AC Q66135;

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DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain Banana) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117120;
RN [1]
RP SEQUENCE FROM N.A.
RA Gafny R., Wexler A., Mawassi M., Israeli Y., Bar-Joseph M.;
RT "Natural infection of banana by a satellite-containing strain of
RL cucumber mosaic virus."
RT Phytoparasitica 24:49-56(1996).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.
CC -----
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CC -----
DR EMBL; U43888; AAA87044.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24174 MW; 9EB4FCB212A21223 CRC64;

Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 218;
Matches 14; Conservativity 100.0%; Pred. No. 3.7e-07; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 7
COAT_CMVC7 STANDARD; PRT; 218 AA.
AC 040983;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain C7-2) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117117;
RN [1]
RP SEQUENCE FROM N.A.
RA Chaumplik P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,
RT "Six new subgroup I members of Japanese cucumber mosaic virus as
RT determined by nucleotide sequence analysis on RNA3's cDNAs.";
RT Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).
RL Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.
CC -----
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DR EMBL; D42079; BAA07675.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24033 MW; 16D96022D1A26FD8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 218;
Matches 14; Conservativity 100.0%; Pred. No. 3.7e-07; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 8
COAT_CMVCS STANDARD; PRT; 218 AA.
ID COAT_CMVCS
AC Q66143;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain CS) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117109;
RN [1]
RP SEQUENCE FROM N.A.
RA Chaumplik P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,
RA Suzuki K., Mise K., Inouye N., Okuno T., Furusawa I.;
RT "Six new subgroup I members of Japanese cucumber mosaic virus as
RT determined by nucleotide sequence analysis on RNA3's cDNAs.";
RT Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).
RL Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.
CC -----
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CC -----
DR EMBL; D28489; BAA05851.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24157 MW; 76F6BDCD9628F683 CRC64;

Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 218;
Matches 14; Conservativity 100.0%; Pred. No. 3.7e-07; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 9
COAT_CMVFC STANDARD; PRT; 218 AA.
ID COAT_CMVFC
AC Q00259;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
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DE Coat protein (Capsid protein) (CP).
OS Cucumber mosaic virus (strain FC) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=31717;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013983; PubMed=1919534;
RA Shintaku M.;
RT "Coat protein gene sequences of two cucumber mosaic virus strains
RT reveal a single amino acid change correlating with chlorosis
RT induction.";
RL J. Gen. Virol. 72:2587-2589(1991).

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DR EMBL; D10544; BAA01403.1; -.
DR PIR; JQ1253; JQ1253.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24130 MW; C4B7CFB12F2A7CAB CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNRR 14
DB 1 MDKSESTSGRNRR 14

RESULT 10
COAT_CMVFT STANDARD; PRT; 218 AA.
ID COAT_CMVFT
AC Q66140;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumber mosaic virus (strain FT) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117112;
RN [1]
RP SEQUENCE FROM N.A.
RA Chaumplik P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,
RA Suzuki K., Mise K., Inouye N., Okuno T., Furusawa I.;
RT "Six new subgroup I members of Japanese cucumber mosaic virus as
RT determined by nucleotide sequence analysis on RNAs' s cDNAs.";
RL Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.

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DR EMBL; D28487; BAA05847.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.

DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24160 MW; 5D3B98298EEA3997 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNRR 14
DB 1 MDKSESTSGRNRR 14

RESULT 11
COAT_CMV11 STANDARD; PRT; 218 AA.
ID COAT_CMV11
AC P14767;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumber mosaic virus (strain I17F) (CMV).
OS Cucumber mosaic virus (strain FNY) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=12308, 12307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=I17F;
RX MEDLINE=90098885; PubMed=2602158;
RA Noel M.J.T., Ben Tahar S.;
RT "Nucleotide sequence of the coat protein gene and flanking regions of
RT cucumber mosaic virus (CMV) strain I17F.";
RL Nucleic Acids Res. 17:10492-10492(1989).
RN [2]
RP ERRATUM.
RX MEDLINE=90206832; PubMed=2320436;
RA Noel M.J.T., Ben Tahar S.;
RL Nucleic Acids Res. 18:1332-1332(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FNY;
RX MEDLINE=91037954; PubMed=2230731;
RA Owen J., Shintaku M., Aeschleman P., Tahar S., Palukaitis P.;
RT "Nucleotide sequence and evolutionary relationships of cucumber mosaic
RT virus (CMV) strains: CMV RNA 3.";
RL J. Gen. Virol. 71:2243-2249(1990).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
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DR EMBL; X16386; CAA34422.1; -.
DR EMBL; D10538; BAA01397.1; -.
DR PIR; S09663; S09663.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24140 MW; C4B4FCB21F197F98 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;

Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
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1 MDKSESTSAGRNR 14

Db 1 MDKSESTSAGRNR 14

RESULT 12
COAT_CMVII STANDARD; PRT; 218 AA.

ID COAT_CMVII STANDARD; PRT; 218 AA.
AC Q83271;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain Iizuka) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117113;
RN [1]
RP SEQUENCE FROM N.A.
RA Karasawa A., Ito A., Okada I., Hase S., Ehara Y.;
RT "A possible role of RNA 2 of cucumber mosaic cucumovirus as a
determinant of infection phenotype on cowpea.";
RL Ann. Phytopathol. Soc. Jpn. 63:289-297(1997).
CC -!- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
family.

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CC EMBL; D16405; BAA03889.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24144 MW; 087CFBFCDE90B6EB CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||||
1 MDKSESTSAGRNR 14

Db 1 MDKSESTSAGRNR 14

RESULT 13
COAT_CMVKO STANDARD; PRT; 218 AA.

ID COAT_CMVKO STANDARD; PRT; 218 AA.
AC Q83269;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain Kor) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim S.J., Cho H.S., Yu J.S., Kwon C.S., Kwon S.Y., Park E.K.,
RA Paek K.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein

CC family.
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CC EMBL; L36251; AAA46418.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24138 MW; 04A21106D3D43344 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||||
1 MDKSESTSAGRNR 14

Db 1 MDKSESTSAGRNR 14

RESULT 14
COAT_CVMV STANDARD; PRT; 218 AA.

ID COAT_CVMV STANDARD; PRT; 218 AA.
AC Q00260;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain M) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=31718;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91037954; PubMed=2230731;
RA Owen J., Shintaku M., Aeschleman P., Tahar S., Palukaitis P.;
RT "Nucleotide sequence and evolutionary relationships of cucumber mosaic
virus (CMV) strains: CMV RNA 3.";
RL J. Gen. Virol. 71:2243-2249(1990).
CC -!- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
family.

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CC EMBL; D10539; BAA01399.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24243 MW; 75B0BFEB247C93D7 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
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1 MDKSESTSAGRNR 14

Db 1 MDKSESTSAGRNR 14

RESULT 15

COAT_CMVN

ID COAT_CMVN STANDARD; PRT; 218 AA.

AC 066138;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Coat protein (Capsid protein) (CP).

OS Cucumbers mosaic virus (strain N) (CMV).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;

OC Cucumovirus.

OK NCBI_TaxID=117123;

OK [1]

RP SEQUENCE FROM N.A.

RA Chaumplik P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,

RA Suzuki K., Mise K., Inoue N., Okuno T., Furusawa I.;

RT "Six new subgroup I members of Japanese cucumber mosaic virus as

determined by nucleotide sequence analysis on RNA's cDNAs.";

RL Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).

CC -!- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein

family.

CC -----

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CC -----

DR EMBL; D28486; BAA05845.1; -.

DR InterPro; IPR000247; Cucumovirus_coat.

DR InterPro; IPR008975; Viral_cap_coat.

DR Pfam; PF00760; Cucumo_coat; 1.

DR PRINTS; PR00222; CUCUMOCOAT.

DR ProDom; PD001284; Cucumovirus_coat; 1.

KW Coat protein.

SQ SEQUENCE 218 AA; 24078 MW; 0BA67C84D8F41B22 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;

Best Local Similarity 100.0%; Pred.No. 3.7e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14

Db 1 MDKSESTSAGRNR 14

Search completed: December 5, 2004, 08:16:51
Job time : 93 secs

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OM protein - protein search, using sw model

Run on: December 5, 2004, 08:08:02 ; Search time 22 Seconds
(without alignments)
42.202 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 14
Sequence: 1 MDKSESTSAGRNR 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	217	6	5422259-2 Patent No. 5422259
2	14	100.0	218	1	US-08-398-209-2 Sequence 2, Appli
3	14	100.0	218	1	US-08-398-209-4 Sequence 4, Appli
4	14	100.0	218	2	US-08-553-619B-3 Sequence 3, Appli
5	14	100.0	218	3	US-08-875-233-2 Sequence 2, Appli
6	14	100.0	218	3	US-08-875-233-4 Sequence 4, Appli
7	14	100.0	218	3	US-08-875-233-6 Sequence 6, Appli
8	14	100.0	218	3	US-08-875-233-15 Sequence 15, Appli
9	14	100.0	218	3	US-09-127-742-2 Sequence 2, Appli
10	14	100.0	218	3	US-09-127-742-4 Sequence 4, Appli
11	14	100.0	218	6	5422259-4 Patent No. 5422259
12	12	85.7	218	3	US-08-875-233-10 Sequence 10, Appli
13	6	42.9	82	4	US-09-252-991A-22748 Sequence 22748, A
14	6	42.9	116	4	US-09-513-999C-7876 Sequence 7876, Ap
15	6	42.9	146	4	US-09-252-991A-24703 Sequence 24703, A
16	6	42.9	203	4	US-09-252-991A-22678 Sequence 22678, A
17	6	42.9	246	4	US-09-252-991A-30490 Sequence 30490, A
18	6	42.9	258	4	US-09-252-991A-22452 Sequence 22452, A
19	6	42.9	264	1	US-08-188-582-26 Sequence 26, Appli
20	6	42.9	264	1	US-08-646-715-26 Sequence 26, Appli
21	6	42.9	264	4	US-09-538-092-1355 Sequence 1355, Ap
22	6	42.9	310	4	US-09-252-991A-23384 Sequence 23384, A
23	6	42.9	373	4	US-09-252-991A-24381 Sequence 24381, A
24	6	42.9	462	4	US-09-252-991A-31817 Sequence 31817, A
25	6	42.9	516	4	US-09-252-991A-17933 Sequence 17933, A
26	6	42.9	521	4	US-09-252-991A-25791 Sequence 25791, A
27	6	42.9	532	4	US-09-248-796A-19478 Sequence 19478, A

28	6	42.9	561	4	US-09-812-079A-2	Sequence 2, Appli
29	6	42.9	576	4	US-09-252-991A-23246	Sequence 23246, A
30	6	42.9	579	4	US-09-171-699-6	Sequence 6, Appli
31	6	42.9	579	4	US-09-171-699-8	Sequence 8, Appli
32	6	42.9	631	1	US-08-605-541B-12	Sequence 12, Appli
33	6	42.9	642	4	US-09-248-796A-19191	Sequence 19191, A
34	6	42.9	663	4	US-09-194-468A-30	Sequence 30, Appli
35	6	42.9	735	4	US-09-252-991A-18657	Sequence 18657, A
36	6	42.9	1011	4	US-09-252-991A-32419	Sequence 32419, A
37	6	42.9	1466	4	US-09-252-991A-30085	Sequence 30085, A
38	6	42.9	2137	3	US-09-134-001C-4463	Sequence 4463, Ap
39	5	35.7	9	1	US-08-615-181-93	Sequence 93, Appli
40	5	35.7	10	1	US-08-090-193-36	Sequence 36, Appli
41	5	35.7	10	2	US-08-488-031-36	Sequence 36, Appli
42	5	35.7	10	2	US-08-486-569-36	Sequence 36, Appli
43	5	35.7	10	2	US-08-488-027-36	Sequence 36, Appli
44	5	35.7	10	2	US-08-090-192-36	Sequence 36, Appli
45	5	35.7	10	2	US-08-482-663-36	Sequence 36, Appli

ALIGNMENTS

RESULT 1
5422259-2
; Patent No. 5422259
; APPLICANT: DE BOTH, MICHEL, BEN TAHAR, SOPHIA, NOEL, MARIANNE;
; PERRET, JOEL
; TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE
; SPECIES CUCUMIS MELO
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/27, 563
; FILING DATE: 05-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566, 255
; FILING DATE: 13-AUG-1990
; SEQ ID NO: 2:
; LENGTH: 217
5422259-2

Query Match 100.0%; Score 14; DB 6; Length 217;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 2
US-08-398-209-2
; Sequence 2, Application US/08398209
; Patent No. 5789656
; GENERAL INFORMATION:
; APPLICANT: Deboth, Michiel
; APPLICANT: No. 57896561, Marianne
; APPLICANT: Ben Tahar, Sophia
; APPLICANT: Perret, Joel
; TITLE OF INVENTION: Transgenic Plants Belonging to the
; TITLE OF INVENTION: Species Cucumis Melo
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5789656west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,209
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,563
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/566,255
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 8910848
FILING DATE: 11-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A.
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.21US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-398-209-2

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 3
US-08-398-209-4
Sequence 4, Application US/08398209
Patent No. 5789656
GENERAL INFORMATION:
APPLICANT: Deboth, Michiel
APPLICANT: No. 57896561, Marianne
APPLICANT: Ben Tahar, Sophia
APPLICANT: Perret, Joel
TITLE OF INVENTION: Transgenic Plants Belonging to the
TITLE OF INVENTION: Species Cucumis Melo
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5789656west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,209
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,563
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/566,255
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 8910848
FILING DATE: 11-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A.
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.21US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-398-209-4

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 4
US-08-553-619B-3
Sequence 3, Application US/08553619B
Patent No. 5919705
GENERAL INFORMATION:
APPLICANT: Dehaan, Petrus T.
TITLE OF INVENTION: Virus Resistant Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5919705artis Crop Protection
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,619B
FILING DATE: December 1, 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 137-1082/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/354-3588
TELEFAX: 415/857-1125
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-619B-3

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

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RESULT 5
US-08-875-233-2
; Sequence 2, Application US/08875233
; Patent No. 6127601
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell
; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-233-2

Query Match      100.0%; Score 14; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDKSESTSAGRNR 14
Db      1 MDKSESTSAGRNR 14

RESULT 6
US-08-875-233-4
; Sequence 4, Application US/08875233
; Patent No. 6127601
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell
; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
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; CURRENT APPLICATION DATA:
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; FILING DATE: 26-JUN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-233-4

Query Match      100.0%; Score 14; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDKSESTSAGRNR 14
Db      1 MDKSESTSAGRNR 14

RESULT 7
US-08-875-233-6
; Sequence 6, Application US/08875233
; Patent No. 6127601
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell
; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-233-6

Query Match      100.0%; Score 14; DB 3; Length 218;

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Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 8

US-08-875-233-15
; Sequence 15, Application US/08875233
; Patent No. 6127601

GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-15

Query Match 100.0%; Score 14; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 9

US-09-127-742-2
; Sequence 2, Application US/09127742A
; Patent No. 6198022

GENERAL INFORMATION:

APPLICANT: DE BOTH, MICHAEL
APPLICANT: NOEL, MARIANNE
APPLICANT: TAHAR, SOPHIA BEN
APPLICANT: PERRET, JOEL
APPLICANT: BIOSEM

TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE SPECIES CUCUMIS MELO
FILE REFERENCE: 8076.21USD2
CURRENT APPLICATION NUMBER: US/09/127,742A
CURRENT FILING DATE: 1998-08-03

EARLIER APPLICATION NUMBER: 08/398,209
EARLIER FILING DATE: 1995-03-02
EARLIER APPLICATION NUMBER: 08/027,563
EARLIER FILING DATE: 1993-03-05
EARLIER APPLICATION NUMBER: 07/566,255
EARLIER FILING DATE: 1990-08-13
EARLIER APPLICATION NUMBER: FR 89 10848
EARLIER FILING DATE: 1989-08-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 218
TYPE: PRT
ORGANISM: cucumber mosaic virus
US-09-127-742-2

Query Match 100.0%; Score 14; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 10

US-09-127-742-4
; Sequence 4, Application US/09127742A
; Patent No. 6198022

GENERAL INFORMATION:
APPLICANT: DE BOTH, MICHAEL
APPLICANT: NOEL, MARIANNE
APPLICANT: TAHAR, SOPHIA BEN
APPLICANT: PERRET, JOEL
APPLICANT: BIOSEM

TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE SPECIES CUCUMIS MELO
FILE REFERENCE: 8076.21USD2
CURRENT APPLICATION NUMBER: US/09/127,742A
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: 08/398,209
EARLIER FILING DATE: 1995-03-02
EARLIER APPLICATION NUMBER: 08/027,563
EARLIER FILING DATE: 1993-03-05
EARLIER APPLICATION NUMBER: 07/566,255
EARLIER FILING DATE: 1990-08-13
EARLIER APPLICATION NUMBER: FR 89 10848
EARLIER FILING DATE: 1989-08-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 218
TYPE: PRT
ORGANISM: cucumber mosaic virus
US-09-127-742-4

Query Match 100.0%; Score 14; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 11

5422259-4
; Patent No. 5422259

APPLICANT: DE BOTH, MICHAEL, BEN TAHAR, SOPHIA, NOEL, MARIANNE;
PERRET, JOEL
TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE
SPECIES CUCUMIS MELO
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/27,563
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 566,255
FILING DATE: 13-AUG-1990
SEQ ID NO:4
LENGTH: 218
5422259-4

Query Match 100.0%; Score 14; DB 6; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 12
US-08-875-233-10
Sequence 10, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-10

Query Match 85.7%; Score 12; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 12
Db 1 MDKSESTSAGRNR 12

RESULT 13
US-09-252-991A-22748
Sequence 22748, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22748
LENGTH: 82
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22748

Query Match 42.9%; Score 6; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AGRNR 14
Db 36 AGRNR 41

RESULT 14
US-09-513-999C-7876
Sequence 7876, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7876
LENGTH: 116
TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: SIGNAL
LOCATION: -19...-1
OTHER INFORMATION: score 5.8
OTHER INFORMATION: seq HLMSTVSTASA/SA
FEATURE:
NAME/KEY: UNSURE
LOCATION: 62
OTHER INFORMATION: Xaa= * or Cys or Trp
FEATURE:
NAME/KEY: UNSURE
LOCATION: 79
OTHER INFORMATION: Xaa=Leu or Trp
FEATURE:
NAME/KEY: UNSURE
LOCATION: 81
OTHER INFORMATION: Xaa=Arg or Ser
US-09-513-999C-7876

Query Match 42.9%; Score 6; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TSAGRNR 12
Db 7 TSAGRNR 12

Db 63 TSAGRN 68

RESULT 15

US-09-252-991A-24703
; Sequence 24703, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24703
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24703

Query Match 42.9%; Score 6; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AGRNRR 14
|||
Db 131 AGRNRR 136

Search completed: December 5, 2004, 08:17:48
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2004, 08:07:32 ; Search time 21 Seconds
(without alignments)
64.145 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 14
Sequence: 1 MDKSESTSAGRNR 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 79:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14	100.0	218	1	JQ1253	coat protein - cuc
2	14	100.0	218	1	JQ1254	coat protein - cuc
3	14	100.0	218	1	JS0090	coat protein - cuc
4	14	100.0	218	1	VCVXY1	coat protein - cuc
5	14	100.0	218	2	JC6075	coat protein - cuc
6	14	100.0	218	2	S42098	coat protein - cuc
7	14	100.0	218	2	S58039	coat protein - cuc
8	14	100.0	218	2	JC6074	coat protein - cuc
9	14	100.0	218	2	JC6073	coat protein - cuc
10	14	100.0	218	2	S09663	coat protein - cuc
11	12	85.7	218	1	JA0136	coat protein - cuc
12	7	50.0	218	2	D71392	coat protein - cuc
13	6	42.9	108	2	JQ2176	hypothetical 11.5K
14	6	42.9	133	2	T17609	hypothetical prote
15	6	42.9	136	2	T47771	hypothetical prote
16	6	42.9	163	2	JQ0139	hypothetical 17.8K
17	6	42.9	174	2	S28733	hypothetical prote
18	6	42.9	202	2	T08230	hypothetical prote
19	6	42.9	226	2	T24125	hypothetical prote
20	6	42.9	228	2	E83109	hypothetical prote
21	6	42.9	264	2	I39141	transcription fact
22	6	42.9	268	2	T24118	hypothetical prote
23	6	42.9	270	2	T24126	hypothetical prote
24	6	42.9	351	2	E87451	conserved hypotet
25	6	42.9	436	2	T00756	hypothetical prote
26	6	42.9	445	2	E84714	probable protein k
27	6	42.9	449	2	E97428	chemotaxis motD pr
28	6	42.9	449	2	AF2646	chemotaxis MotD pr
29	6	42.9	496	2	T34760	oligopeptide ABC t

30	6	42.9	497	2	T33634	hypothetical prote
31	6	42.9	561	1	WMBETW	65K lower matrix p
32	6	42.9	561	1	WMBE65	65K lower matrix p
33	6	42.9	662	2	A42496	gelatinase A (EC 3
34	6	42.9	662	2	S34780	gelatinase A (EC 3
35	6	42.9	663	1	S46492	gelatinase A (EC 3
36	6	42.9	742	2	H95270	probable kinase/es
37	6	42.9	1006	2	T13331	probable tail prot
38	6	42.9	1143	2	T28129	hypothetical prote
39	6	42.9	1275	2	T33369	hypothetical prote
40	6	42.9	1750	2	E86151	hypothetical prote
41	6	42.9	2160	2	T20241	hypothetical prote
42	6	42.9	2570	2	T17451	fimbriae-associate
43	6	42.9	2693	2	A40743	IP3 receptor, XIP3
44	6	42.9	3562	2	A47171	chondroitin sulfat
45	5	35.7	26	2	S04376	hypothetical prote

ALIGNMENTS

RESULT 1
JQ1253
coat protein - cucumber mosaic virus (strain FC)
C/Species: cucumber mosaic virus, CMV
C/Date: 31-Mar-1992 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C/Accession: JQ1253
R/Shintaku, M.
J. Gen. Virol. 72, 2587-2589, 1991
A/Title: Coat protein gene sequences of two cucumber mosaic virus strains reveal a single
A/Reference number: JQ1253; MUID:92013983; PMID:1919534
A/Accession: JQ1253
A/Molecule type: genomic RNA
A/Residues: 1-218 <SHI>
A/Cross-references: UNIPROT:Q00259; GB:D10544; MID:g222024; PIDN:BA01403.1; PID:g222025
A/Note: comparison of the amino acid sequence of this protein to that of strain P6 shows
R/Tsunasawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A/Title: Micro-identification of amino-terminal acetyl amino acids in proteins.
A/Reference number: A61297; MUID:83056735; PMID:6754709
A/Contents: annotation; acetylation
C/Comment: This cucumber mosaic virus strain induces a yellow chlorosis.
C/Superfamily: cucumber mosaic virus coat protein
C/Keywords: acetylated amino end; coat protein
F/1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 2
JQ1254
coat protein - cucumber mosaic virus (strain P6)
C/Species: cucumber mosaic virus, CMV
C/Date: 31-Mar-1992 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C/Accession: JQ1254
R/Shintaku, M.
J. Gen. Virol. 72, 2587-2589, 1991
A/Title: Coat protein gene sequences of two cucumber mosaic virus strains reveal a single
A/Reference number: JQ1253; MUID:92013983; PMID:1919534
A/Accession: JQ1254
A/Molecule type: genomic RNA
A/Residues: 1-218 <SHI>
A/Cross-references: UNIPROT:Q00261; GB:D10545; MID:g222026; PIDN:BA01404.1; PID:g222027
A/Note: comparison of the amino acid sequence of this protein to that of strain FC shows
R/Tsunasawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A/Title: Micro-identification of amino-terminal acetyl amino acids in proteins.

A;Reference number: A61297; MUID:83056735; PMID:6754709
A;Contents: annotation; acetylation
C;Comment: This cucumber mosaic virus strain induces a yellow chlorosis.
C;Superfamily: cucumber mosaic virus coat protein
C;Keywords: acetylated amino end; coat protein
F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 3
JS0090
coat protein - cucumber mosaic virus (strain O)
C;Species: cucumber mosaic virus, CMV
C;Date: 31-Mar-1992 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C;Accession: JS0090; PS0314
R;Hayakawa, T.; Mizukami, M.; Nakajima, M.; Suzuki, M.
J. Gen. Virol. 70, 499-504, 1989
A;Title: Complete nucleotide sequence of RNA 3 from cucumber mosaic virus (CMV) strain C
A;Reference number: JS0089; MUID:89279231; PMID:2732698
A;Accession: JS0090
A;Molecule type: mRNA
A;Residues: 1-218 <HAY>

A;Cross-references: UNIPROT:P16489; GB:D00385; NID:g222030; PIDN:BAA00297.1; PID:g222032
A;Accession: PS0314
A;Molecule type: protein
A;Residues: 216-218 <HA2>
R;Tsunasawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A;Title: Micro-identification of amino-terminal acetyl amino acids in proteins.
A;Reference number: A61297; MUID:83056735; PMID:6754709
A;Contents: annotation; acetylation
C;Genetics:
A;Map position: segment 3
C;Superfamily: cucumber mosaic virus coat protein
C;Keywords: acetylated amino end; coat protein
F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 4
VCVXY1

coat protein - cucumber mosaic virus (strain Y)
C;Species: cucumber mosaic virus, CMV
A;Note: host Nicotiana tabacum cv. Xanthi nc (tobacco)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: JA0097
R;Nitta, N.; Masuta, C.; Kuwata, S.; Takanami, Y.
Ann. Phytopathol. Soc. Jpn. 54, 516-522, 1989
A;Title: Comparative studies on the nucleotide sequence of cucumber mosaic virus RNA3 be
A;Reference number: JA0096
A;Accession: JA0097
A;Molecule type: mRNA
A;Residues: 1-218 <NIT>
A;Cross-references: UNIPROT:P18027
R;Tsunasawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A;Title: Micro-identification of amino-terminal acetyl amino acids in proteins.
A;Reference number: A61297; MUID:83056735; PMID:6754709
A;Contents: annotation; acetylation

C;Comment: The genome consists of three single-stranded, positive RNAs, designated RNA1,
C;Genetics:
A;Map position: segment RNA3
C;Superfamily: cucumber mosaic virus coat protein
C;Keywords: acetylated amino end; coat protein
F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 5
JC6075
coat protein - cucumber mosaic virus (strain CS)
C;Species: cucumber mosaic virus, CMV
C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC6075
R;Huaping, L.; Hu, J.S.; Barry, K.; Hweichung, F.
Chinese J. Virol. 12, 235-242, 1996
A;Title: Coat protein gene sequence analysis of three cucumber mosaic virus strains infec
A;Reference number: JC6073
A;Accession: JC6075
A;Molecule type: mRNA
A;Residues: 1-218 <HUA>

A;Cross-references: UNIPROT:Q8JFX2; UNIPROT:Q9DJX2; UNIPROT:Q91PK5; UNIPROT:Q9DJX3; UNIP
ROT:Q8JFX0; UNIPROT:Q9DJW5; UNIPROT:Q91PP6; UNIPROT:Q9JFY4; UNIPROT:Q8JFX4; UNIPROT:Q9D
6132; UNIPROT:Q9YJS2; UNIPROT:Q8JFW8; UNIPROT:Q9JENS6; UNIPROT:Q8J259; UNIPROT:Q9DWW2; UN
A;Experimental source: strain CS
A;Note: the authors translated the codon CCG for residue 83 as Gly
C;Genetics:
A;Gene: cp
C;Superfamily: cucumber mosaic virus coat protein
C;Keywords: coat protein

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 6
S42098
coat protein - cucumber mosaic virus
C;Species: cucumber mosaic virus, CMV
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S42098
R;Hyon, S.; Park, Y.I.
submitted to the EMBL Data Library, February 1994
A;Description: Nucleotide sequence of cDNA from RNA4 of cucumber mosaic virus-As the Kore
A;Reference number: S42098
A;Accession: S42098
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-218 <HYO>
A;Cross-references: UNIPROT:Q66154; EMBL:X77855; NID:g457166; PIDN:CAA54846.1; PID:g45716
C;Superfamily: cucumber mosaic virus coat protein

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 7

S58039
capsid protein - cucumber mosaic virus
C/Species: cucumber mosaic virus, CMV
C/Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S58039
R/Haq, Q.M.R.
submitted to the EMBL Data Library, July 1995
A/Reference number: S58039
A/Accession: S58039
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-218 <HAQ>
A/Cross-references: UNIPROT:Q66157; EMBL:X89652; NID:g902619; PIDN:CAA61802.1; PID:g9026
C/Superfamily: cucumber mosaic virus coat protein

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 8

JC6074
coat protein - cucumber mosaic virus (strain MM)
C/Species: cucumber mosaic virus, CMV
C/Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C/Accession: JC6074
R/Huaping, L.; Hu, J.S.; Barry, K.; Hweichung, F.
Chinese J. Virol. 12, 235-242, 1996
A/Title: Coat protein gene sequence analysis of three cucumber mosaic virus strains infe
A/Reference number: JC6073
A/Accession: JC6074
A/Molecule type: mRNA
A/Residues: 1-218 <HUA>
A/Cross-references: UNIPROT:Q83257; UNIPROT:O55251; UNIPROT:Q9WAB3; UNIPROT:Q9YJR9; UNIF
A/Experimental source: strain MM
A/Note: the authors translated the codon CGT for residue 30 as Ala
C/Genetics:
A/Gene: cp.
C/Superfamily: cucumber mosaic virus coat protein
C/Keywords: coat protein

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 9

JC6073
coat protein - cucumber mosaic virus (strain BS)
C/Species: cucumber mosaic virus, CMV
C/Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C/Accession: JC6073
R/Huaping, L.; Hu, J.S.; Barry, K.; Hweichung, F.
Chinese J. Virol. 12, 235-242, 1996
A/Title: Coat protein gene sequence analysis of three cucumber mosaic virus strains infe
A/Reference number: JC6073
A/Accession: JC6073
A/Molecule type: mRNA
A/Residues: 1-218 <HUA>
A/Cross-references: UNIPROT:Q9DJW8; UNIPROT:Q9YJR7; UNIPROT:Q8JFX1; UNIPROT:Q9E2V6; UNIF
PROT:Q91PP6; UNIPROT:Q9JFY4; UNIPROT:Q66157; UNIPROT:Q66130; UNIPROT:Q8JFX4; UNIPROT:Q9D
6132; UNIPROT:Q9YJS2; UNIPROT:Q8JFW8; UNIPROT:Q9ENS6; UNIPROT:Q83259; UNIPROT:Q9DWM2; UN
A/Experimental source: strain BS

A/Note: the authors translated the codon CCA for residue 56 as Thr and CCC for residue 5;
C/Genetics:
A/Gene: cp
C/Superfamily: cucumber mosaic virus coat protein
C/Keywords: coat protein

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 10

S09663
coat protein - cucumber mosaic virus (strain I17F)
C/Species: cucumber mosaic virus, CMV
A/Variety: strain I17F
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S09663; S06932
R/Noel, M.J.T.; Tahar, S.B.
Nucleic Acids Res. 18, 1332, 1990
A/Title: Corrigendum. Nucleotide sequence of the coat protein gene and flanking regions
A/Reference number: S09663; MUID:90206832; PMID:2320436
A/Accession: S09663
A/Molecule type: mRNA
A/Residues: 1-218 <NOE>
A/Cross-references: UNIPROT:P14767
A/Experimental source: strain I17F
A/Note: this is a revision to the sequence from reference S06932
R/Noel, M.J.T.; Tahar, S.B.
Nucleic Acids Res. 17, 10492, 1989
A/Title: Nucleotide sequence of the coat protein gene and flanking regions of Cucumber Mc
A/Reference number: S06932; MUID:90098885; PMID:2602158
A/Accession: S06932
A/Molecule type: mRNA
A/Residues: 1-6,'W',8-44,'W',46-51,'W',53-56,'W',58-68,'W',70,'W',72-73,'W',75-96,'W',98-
A/Cross-references: EMBL:X16386
A/Experimental source: strain I17F
A/Note: this sequence has been revised in reference S09663
C/Superfamily: cucumber mosaic virus coat protein

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
|||||
Db 1 MDKSESTSAGRNR 14

RESULT 11

JA0136
coat protein - cucumber mosaic virus (strain C)
C/Species: cucumber mosaic virus, CMV
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: JA0136
R/Quemada, H.; Kearney, C.; Gonsalves, D.; Slightom, J.L.
J. Gen. Virol. 70, 1065-1073, 1989
A/Title: Nucleotide sequences of the coat protein genes and flanking regions of cucumber
A/Reference number: JU0087; MUID:89279284; PMID:2732712
A/Accession: JA0136
A/Molecule type: genomic RNA
A/Residues: 1-218 <QUE>
A/Cross-references: UNIPROT:P21368; GB:D00462; NID:g2222041; PIDN:BAA00357.1; PID:g2222042
R/Tsunasawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A/Title: Micro-identification of amino-terminal acetyl amino acids in proteins.
A/Reference number: A61297; MUID:83056735; PMID:6754709
A/Contents: annotation; acetylation
C/Genetics:

A;Map position: segment RNA3
C;Superfamily: cucumber mosaic virus coat protein
C;Keywords: acetylated amino end; coat protein; glycoprotein
F;1/Modified site: acetylated amino end (Met) #status experimental
F;43/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.7%; Score 12; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGR 12
|||||
Db 1 MDKSESTSAGR 12

RESULT 12
D71392
coat protein - cucumber mosaic virus (strain Ixora)
N;Alternate names: capsid protein

C;Species: cucumber mosaic virus, CMV
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Accession: D71392
R;McGarvey, P.; Touseignant, M.; Gelecka, L.; Cellini, F.; Kaper, J.M.
J. Gen. Virol. 76, 2257-2270, 1995
A;Title: The complete sequence of a cucumber mosaic virus from Ixora that is deficient i
A;Reference number: A71392; MUID:96005047; PMID:7561763
A;Accession: D71392

A;Molecule type: mRNA
A;Residues: 1-218 <MG>
A;Cross-references: UNIPROT:Q66120; GB:U20219; NID:g1161916; PIDN:AAC54619.1; PID:g11619
A;Experimental source: strain Ixora
C;Comment: The CMV genome consists of three species of single-stranded, capped, positive
C;Comment: The Ixora strain in unusual in that it does not replicate several well charac
ptoms found when replicated by other CMV strains.
C;Genetics:

A;Map position: segment RNA 3
C;Superfamily: cucumber mosaic virus coat protein
C;Keywords: acetylated amino end; coat protein
F;1/Modified site: acetylated amino end (Met) #status predicted

Query Match 50.0%; Score 7; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SAGRNR 14
|||||
Db 8 SAGRNR 14

RESULT 13
JQ2176
hypothetical 11.5K protein (clone GV-B) - garlic virus B
N;Alternate names: hypothetical protein II
C;Species: garlic virus B
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C;Accession: JQ2176; S27912
R;Sumi, S.; Tsuneyoshi, T.; Furutani, H.
J. Gen. Virol. 74, 1879-1885, 1993
A;Title: Novel rod-shaped viruses isolated from garlic, Allium sativum, possessing a uni
A;Reference number: JQ2171; MUID:93389442; PMID:8376963
A;Accession: JQ2176

A;Molecule type: mRNA
A;Residues: 1-108 <SUM>
A;Cross-references: UNIPROT:Q67695; GB:AB010301; GB:D11158; NID:g2826152; PIDN:BAA61814.
R;Sumi, S.I.
submitted to the EMBL Data Library, July 1992
A;Reference number: S27908
A;Accession: S27912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <SU2>

A;Cross-references: EMBL:D11158; NID:g221432; PIDN:BAA61814.1; PID:g221433
C;Superfamily: barley stripe mosaic virus 14K protein

Query Match 42.9%; Score 6; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SESTSA 9
|||||
Db 100 SESTSA 105

RESULT 14
T17609
hypothetical protein a119L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17609

R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T17609

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-133 <GRA>
A;Cross-references: UNIPROT:Q84440; EMBL:U42580; NID:g4028896; PIDN:AAC96487.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: a119L

Query Match 42.9%; Score 6; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 STSAGR 11
|||||
Db 128 STSAGR 133

RESULT 15
T47771
hypothetical protein F2413.190 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47771
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24475
A;Accession: T47771
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <NYA>
A;Cross-references: UNIPROT:Q9M119; EMBL:AL138655
A;Experimental source: cultivar Columbia; BAC clone F2413
C;Genetics:
A;Map position: 3
A;Note: F2413.190
C;Superfamily: Arabidopsis thaliana hypothetical protein F2413.190

Query Match 42.9%; Score 6; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SESTSA 9
|||||
Db 6 SESTSA 11

Search completed: December 5, 2004, 08:17:19
Job time : 22 secs